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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AY892761 Synthetic	AY892761	œ	480	86.8	478	œ ;
AY890283 Synthetic	AY890283	8	480	86.8	478	7
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46.8	47.0	47.0	48.1	48.1	49.7	49.7	49.7	49.7	53.7	54.3	67.5	78.0	78.3	78.3	78.3	78.9	78.9	78.9	86.0	86.0	86.5	86.6	86.6	86.8	86.8
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ALIGNMENTS

	source	AUTHORS TITLE JOURNAL FEATURES	REFERENCE AUTHORS TITLE JOURNAL PUBMED	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AF078078
/function="mediates activation of stress-responsive MTKI/MEKK4 MAPKKK" /note="stress-inducible; similar to GADD45" /codon_start=1 /product="growth arrest and DNA-damage-inducible protein GADD45gamma" GADD45gamma" /protein_id="AACB3329.1" /db_xref="GI:3978394" /translation="MTLEEVRGQDTVPESTARMQGAGKALHELLISAQRQGCLTAGVY translation="MTLEEVRGQDTVPESTARMQGAGKALHELLISAQRQGCLTAGVY translation="MTLEEVRGQDTVPESTARMQGAGKALHELLISAQRQGCLTAGVY translation="MTLEEVRGQDTVPESTARMQGAGKALHELLISAQRQGCLTAGVY translation="MTLEEVRGQDTVPESTARMQGAGKALHELLISAQRQGCLTAGVY translation="MTLEEVRGDDFQDLACHFTLIQAFCCENDIDIVRVGDVQRLA AIVGAGEEAGAAPGDLHCILISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE" AIVGAGEEAGAAPGDLHCILISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE"		Takekawa, M. and Saito, H. Takekawa, M. and Saito, H. Direct Submission Submitted (14-JUL-1998) Dana-Parber Cancer Institute, Harvard Medical School, 44 Binney Street, Boston, MA 02115, USA' Location/Qualifiers	Hominidae; Hom6. 1 (Dases 1 to 551) Takekawa,M. and Saito,H. Takekawa,M. and Saito,H. A family of stress-inducible GADD45-like proteins mediate activation of the stress-responsive MTK1/MEKK4 MAPKKK Cell 95 (4), 521-530 (1998) 9827804	iens growth arrest and DNA- mma mRNA, complete cds. 1 GI:3978393 iens (human) iens (human) iens (human) iens (Chordata; Crani a; Metazoa; Euarchontoglire	AF078078 551 bp mRNA linear PRI 06-DEC-1998

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1 (bases 1 to 1065)
Smith, K. A. and Beadling, C.
Nucleic acids encoding CR5 polypeptide, thereof, and expression thereof
Patent: US 5871960-A 11 16-FEB-1999;
Location/Qualifiers
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Smith, K.A. and Beadling, C.
Nucleic acids encoding CR2 polypeptides,
cell thereof, and expression thereof
Patent: US 5871961-A 11 16-FEB-1999;
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/mol_type="unassion
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APO79806 APO79806. APO79806. APO79806.1 GI:4731862 Homo sapiens (human) SM Homo sapiens (human) I (bases I to 1066) SM Homo sapiens (human) SM Homo	AATGTGACCTTCTGTGTGCTGCTGCGGGTGAGGACGACGACGACTCGCGCTGCAG

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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
                                                                                                                                                                                                                                                                                                                                                                                              BC019325 1068 bp mRNA linear I Homo sapiens growth arrest and DNA-damage-inducible, (cDNA clone MGC:4374 IMAGE:2823131), complete cds.
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                   Hominidae; Homo.

1 (bases 1 to 1068)
                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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/translation="MTLEEVRGODTVPESTARMQGAGKALHELLLSAQRQGCLTAGVY
/stanslation="MTLEEVRGDEDIALQHETLIQAFCCEMDIDIVRVGDVQRLA
ESAKVLHVDDDNVTFCVLAAGEEDEGDIALQHETLIQAFCCEMDIDIVRVGDVQRLA
AIVGAGEEAGAPGDLHCILISNPNEDAMKDPALEKLSLFCEESRSVNDWVPSITLPE"
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Pred. No. 6.3e-125;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petecu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalaka,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,B.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,B.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski, M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: c Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mkNA gi: 9790905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (13-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Strausberg, R. L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F. S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Garninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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BC000465.2 GI:33988508
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100.0%; Pred. No. 6.3e-125;
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GADD45gamma"

GADD45-GAMMA,

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Query Match 98.4
Best Local Similarity 100
Matches 542; Conservative

98.4%; Score 542; DB 5; 100.0%; Pred. No. 6.3e-12 tive 0; Mismatches

Length 1077;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.misc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter.N., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Laric,P., Legaspi,R.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web Siter (NISC)
                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.geries: IRAL Plate: 1 Row: j Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9790
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Contact: MGC help desk
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On Aug 20, 2003 this sequence version replaced
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human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                /clone="MGC:8544 IMAGE:2822765"
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                                                      note="Vector: pOTB7"
                                                                                            lab_host="DH10B-R"
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Patent: EP 1394274-A 37 03-MAR-2004;
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Sequence 37 from Patent
CQ776351
CQ776351.1 GI:45379741
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Methods of testing for bronchial asthma or
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larity 100.0%; I
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                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Location/Qualifiers
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                                                                                  98.4%; Score 542; DB 2; Liarity 100.0%; Pred. No. 6.3e-125; Conservative 0; Mismatches 0;
                                                                                                                                                          /mol_type="unassigned
/db_xref="taxon:9606"
                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="unassigned DNA"
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OTSUKA PHARWACEUT CO LTD

OTSUKA PHARWACEUT CO LTD

PN JP 1997206083-A/2

PD 12-AUG-1997

PF 09-FEB-1996 JP 1996023612

PI SUZUKI MIKIO, WATANABE TAKESHT, FUJIWARA TSUTOMU PC

C12N15/09,C07H21/04,C12N1/21,C12P21/02//C07K14/52,(C12N1/21, PC

C12R1:19);

PC (C12P21/02,C12R1:19);

PC (C12P21/02,C12R1:19);

CC strandedness: Double;

CC topology: Linear;

FH Key

FT Source 1..1036

FT Source /organism='Homo sapiens'

FT /ctissue_type='placenta'

FT /CDS 84..563

PT CDS 84..563

PT CDS (84..563
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1 (bases 1 to 1036)
Suzuki,M., Watanabe,T. and Fujiwara,T.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/product='GRP17'.
Location/Qualifiers
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                                                                               and Tanigami,A.

Molecular cloning, expression, and mapping of a novel human cDNA,
GRP17, highly homologous to human gadd45 and murine MyD118
J. Hum. Genet. 44 (5), 300-303 (1999)
                                                                                                                                                                                                                                                                                                                         Homo sapiens GRP17 mRNA
          Watanabe,T.
Direct Submission
Submitted (11-JAN-1996) Takeshi Watanabe, Otsuka
                                                                                                                                                         Suzuki, M., Watanabe, T.K., Fujiwara, T., Nakamura, Yp.6., Takahashi,
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Kawauchi-cho, Tokushima,
Fax:0886-37-1035)
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                                                                                                                                                                                                                                                                                                             GGCGATGTGCAGCGGCTGGCGGCTATCGTGGGCGCCGGCGAGGAGGAGGCGGGTGCGCCGGGC
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/codon_start=1
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/db_xref="GI:5911969"
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ESAKVLAVDPDMVTFCVLAAGEEDEGDIALQIHFTLIQAFCCEKNDIDIVRVGDVQRLA
AIVGAGEEAGAPGDLHCILISNPNEDAMKDPALEKLSLFCEESRSVNDWVPSITLPE"
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-cho, Tokushima, Tokushima 771-01, Japan (Tel:0886-65-2888)
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84. .563
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/db_xref="taxon:9606"
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                       1066 bp DNA from Patent WO02068579.
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Pred. No. 4e-124;
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Best Local Similarity
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AF087883.1
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Homo sapiens growth arrest and I
(GADD45G) mRNA, complete cds.
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority humanexons or transcripts, for detecting expression and characters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent: WO 02068579-A 10234 06-SEP-2002; PE Corporation (NY) (US)
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                                                                                 GGAGAAGCTCAGCCTGTTTTGCGAGGAGAGCCGCAGCGTTAACGACTGGGTGCCCAGCAT
                                                                                                       GGAGAAGCTCAGCCTGTTTTGCGAGGAGAGCCCGCAGCGTTAACGACTGGGTGCCCAGCAT
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CACCCTCCCCGAGTGACAGCCCGGCGGGGACCTTGGTCTGATCGACGTGGTGACGCCCCG
                      CACCCTCCCCGAGTGACAGCCCGGCGGGGGACCTTGGTCTGATCGACGTGGTGACGCCCCG
                                                                                                                                                                    CGACCTGCACTGCATCCTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTT
                                                                                                                                                                                                                                                          GGGCGATGTGCAGCGGCTGGCGGCTATCGTGGGCGCCGGCGAGGAGGCGGGTGCGCCGGG
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 3.6e-122;
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p mRNA linear DNA damage inducible

protein PRI 01-FEB-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assignment of human GADD45G to chromosome radiation hybrid mapping Cytogenet. Cell Genet. 88 (1-2), 95-96 (20 10773677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostômi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 1060)
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                                                                            GACCTGCACTGCATCCTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCCGCCTTG 420
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GAGAAGCTCAGCCTGTTTTGCGAGGAGAGCCGCAGCGTTAACGACTGGGTGCCCAGCATC
            GAGAAGCTCAGCCTGTTTTGCGAGGAGAGCCGCAGCGTTAACGACTGGGTGCCCAGCATC
                                                          GACCTGCACTGCATCCTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTG
                                                                                                                      GGCGATGTGCAGCCGGCTGGCGCTATCGTGGGCGCCGAGGAGGAGGCGAGCTGCGCGTGC
                                                                                                                                                                                ATCCATTTACGCTGATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAK00414.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="growth arrest
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96. .575
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codon_start=1
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Pred. No. 4.5e-122;
0; Mismatches 9;
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Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood ce
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Patent: US 6607879-A 820 19-AUG-2003;
Incyte Corporation; Palo Alto, CA
Location/Qualifiers
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                                 CACCCTCCCCGAGTGACAGCCCGGGGGGCCTTGGTCTGATCGACGTGGTGACGCCCCG
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/mol_type="genomic |
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Pred. No. 2.4e-121;
0; Mismatches 2;
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2 (bases 1 to 480)

2 (bases 1 to 480)

3 (Alnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.

Direct Submission

Albarra, A. Direct Submission

Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the expression clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion (TM) cloning system between the Sall and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              624
                           76 GGTGCCGGGAAAGCGCTGCATGAGTTGCTGCTGTCGGCGCAGCGTCAGGGCTGCCTCACT
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                                                                                                                                                                                                         al Similarity
478; Conserv
61 GGTGCCGGGAAAGCGCTGCATGAGTTGCTGCTGTCGGCGCAGCGTCAGGGCTGCCTCACT
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Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.

Cloning of human full-length CDSs in BD Creator(TM) System Donor
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Homo sapiens growth arrest and DNA-damage-inducible, gamma
complete cds.
BT007234
                                                                                                   1 ATGACTCTGGAAGAAGTCCGCGGCCAGGACACAGTTCCGGAAAGCACAGCCAGGATGCAG
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                 ATGACTCTGGAAGAAGTCCGCGGCCAGGACAGATTCCGGAAAGCACAGCCAGGATGCAG
                                                                                                                                                                                                      86.8%; Score 478; DB 5; Lilarity 100.0%; Pred. No. 7.9e-109; Conservative 0; Mismatches 0;
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/clone_lib="BD Creator(TM) CDS Library derived from MGC
collection"
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ESAKVLNVDPDNVTFCVLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLA
AIVGAGEEAGAPGDLHCILISNPNEDAMKDPALEKLSLFCEESRSVNDWVPSITLPE"
                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="growth arrest and DNA-damage-inducible, gamma"
/protein_ida="AAP35898.1"
/db_xref="GI:30583307"
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH5alpha T1 resistant"
/note="Vector: pDNR-Dual"
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Вb	Ş	В	Ş	DЬ	γQ	Вb	γ	DЬ	γQ	DЬ	8
421 TTTGCGAGGAGACCGCAGCGTTAACGACTGGCTGCCCAGCATCACCCTCCCCGAGT 478	436 TTTTGCGAGGAGAGCCGCAGCGTTAACGACTGGGTGCCCAGCATCACCCCTCCCCGAGT 493	361 CTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCCGCCTTGGAGAAGCTCAGCCTG 420	376 CTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTGGAGAAGCTCAGCCTG 435	301 CTGGCGGCTATCGTGGGCGCGAGGAGGAGGGGGGGGGGG	316 CTGGCGGCTATCGTGGGCGCCGGCGAGGAGGCGGGTGCGCCCGGGCCGACCTGCACTGCATC 375	241 ATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTGGGCGATGTGCAGCGG 300	256 ATCCAGGCTTTCTGCCAGAACGACATCGACATAGTGCGCCGTGGGCGATGTGCAGCCG 315	181 GTGCTGGGTGAGGAGGACGAGGGGGACATCGCGCTGCAGATCCATTTTACGCTG 240	196 GTGCTGGCTGCGGGTGAGGAGGACGACGACGACATCGCGCTGCAGATCCATTTTACGCTG 255	121 GCCGGCGTCTACGAGTCAGCCAAAGTCTTGAACGTGGACCCCGACAATGTGACCTTCTGT 180	136 GCCGGCGTCTACGAGTCAGCCAAAGTCTTGAACGTGGACCCCGACAATGTGACCTTCTGT 195

Search completed: June 4, 2006, 23:10:17 Job time: 5081 secs

GenCore version 5.1.9
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Acn44751 Human mRN	AAA39682 ACN44751	11	1302	86.6	477
Adv43063 Human psy	ADV43063	14	480	87.1	480
	ADQ24782	12	1202	93.1	512.8
Humar	ADQ20819	12	612	95.4	525.4
Human	ADS83561	13	750	95.8	527.8
Humar	ADI31494	11	750	95.8	527.8
Aat74048 Human GRP	AAT74048	N	1036	97.5	537.2
Adx85165 Human gad	ADX85165	14	1078	98.4	542
Adr25449 Breast ca	ADR25449	13	1078	98.4	542
Adj74785 Marker ge	ADJ74785	12	1078	98.4	542
Adp65003 Human gro	ADP65003	11	1078	98.4	542
Acc59049 Human Gad	ACC59049	8	1078	98.4	542
Adp65476 Human cyt	ADP65476	11	1066	98.4	542
Aaa64826 Human SYG	AAA64826	W	1066		542
Aaa39665 Human CR6	AAA39665	W	1065	98.4	542
Aat43381 Human cyt	AAT43381	N	1065	98.4	542
Aed73447 Human pla	AED73447	14	1056	98.4	542
Description	ID	BB	Query Match Length	Query	Score
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	SUMMARIES				

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32.1	32.7	32.7	32.7	32.7	32.7	32.7	32.7	32.7	32.7	32.7	32.7	33.9	49.7	49.7	49.7	53.7	62.4	67.5	73.6	76.9	77.5	78.3	78.3	78.3	78.3	85.7
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ACL55905	ADY16172	ADP24253	AAZ42213	ACN40402	ADQ86723	ADQ83479	ADQ85622	ADQ84244	ADY16174	AED73625	AED07117	ACN44748	ACN44750	ABL56856	AAA64827	ABI99870	AEF75388	AAC59606	ADD34070	ACN44749	ADV77129	ADX85167	ADJ75713	ACC59050	ADZ60283	AAT74047
Ac155905 Human col		PRO		Acn40402 Tumour-as			Human	Human					Human		Aaa64827 Human SYG	Abi99870 Mouse isc	Aef75388 Human pol	Aac59606 Human sec	Add34070 Mouse mit	Acn44749 Mouse mRN				.2	Adz60283 Murine Ga	Aat74047 Human GRP

ALIGNMENTS

RESULT 1
AED73447/c
ID AED73447 standard; cDNA; 1056 BP. pre-eclampsia; gynecological; chromosome-9; ss. Human placental protein encoding cDNA SEQ ID NO:275. WPI; 2005-808574/82. P-PSDB; AED74299. 12-JAN-2006 AED73447; Labat I, (NUVE-) NUVELO INC 07-APR-2003; 2003US-0462047P 07-APR-2004; 2004US-00821234 17-NOV-2005. US2005255114-A1. Homo sapiens Tang YT, (first entry) Stache-Crain B, Boyle B;

Identifying a patient with a higher risk of preeclampsia comprises nucleic acid hybridization assay or antibody assay to determine level of a specific nucleic acid (mRNA) or polypeptide.

Claim 1; SEQ ID NO 275; 358pp; English.

The invention relates to a method for identifying a patient with a higher risk of preeclampsia. The method comprises: (a) assaying a sample from the patient to determine the level of a mRNA or other polynucleotide within the sample that hybridizes specifically to a polynucleotide of AED73173-AED74024, and comparing the level to a standard; or (b) contacting a sample from the patient with an antibody that specifically

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binds to a polypeptide of AED74025-AED74876 to determine the level of polypeptide within the sample, and comparing the level to a standard. Also described: (1) a diagnostic kit, for detecting preeclampsia, comprising: (a) an antibody specific for any of the polypeptides of AED74025-AED74876 or their fragments; or (b) a polymucleotide sequence comprising any of AED73173-AED74024 coupled to a surface; and (c) a standard for any of the polypeptides of AED74025-AED74876 or any of the polypeptides of AED74025-AED74876 or any of the polypeptides of abdrained composition comprising an antibody specific for any of the polypeptides of abdrained sequence or more purified polypeptides of AED74025-AED74876, to ameliorate signs or symptoms of preeclampsia; (2) a pharmaceutical composition comprising or symptoms of preeclampsia; and (3) a method of treating preeclampsia. The composition and method are useful for treating preeclampsia. The composition and method are useful for treating preeclampsia. The present sequence represents a nucleic acid sequence obtained from a human placental cDNA library. Note - The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
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                                                                                                            AAT43381 standard;
11-MAR-1997
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Matches
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05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                      8 Clones (AAT43376-83) contg. interleukin-2 (II-2)-induced genes were isolated from a human IL2 receptor-positive T blast cell cDNA library following II-2 stimulation. 6 Of these ligand-induced genes (CR1, 2, 3, 5, 6, 8) are novel. The CR6 gene encodes a 17.5 kba protein (AAW08138) that may facilitate cellular proliferation by preventing the inhibitory activity of p21. Expression is suppressed by elevated cAMP. CR genes and polypeptides (AAW08133-40) are useful as diagnostic or therapputic agents; CR gene sequences can be used to detect and treat allelic mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine response gene; CR6; interleukin-2; IL-2; ligand-stimulated gene expression; diagnosis; therapy; ss
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1065 BP; 198 A; 293 C; 378 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 29-20; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytokine response proteins and genes - used in the detection of diseases caused by a mutation in the CR coding region.
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                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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GGCGATGTGCAGCGGCTGGCGGCTATCGTGGGCGCCGGCGAGGAGGCGGGTGCGCCGGGC
                                                         ATCCATTTTACGCTGATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTG
                                                                                                              AATGTGACCTTCTGTGTGCTGGCTGCGGGTGAGGACGACGACGGCGACATCGCGCTGCAG
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                                                                                            AATGTGACCTTCTGTGTGCTGCCTGCGGGTGAGGAGGACGAGGGCGACATCGCGCTGCAG
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95US-00462337.
95US-00462390.
95US-00462390.
95US-00463074.
95US-00463081.
95US-00465585.
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                                                                                                                                                                                                                                                                                                                                               98.4%; Score 542; DB 2; L
100.0%; Pred. No. 5.8e-113;
cive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                               196 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                              Length 1065;
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10-AUG-1993;
27-OCT-1994;
05-JUN-1996;
This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine response gene 2 (CR2) and modulates CR2 activity. The products of the invention have cytostatic, anti-allergic, immunosuppressive and antimicrobial activity. The antibodies are useful as therapeutic agents for regulating cellular proliferation and differentiation and for treating all kinds of cancers, immune diseases such as allergic, autoimmune, and rheumatologic diseases, transplant rejection, and as anti-infectives for fighting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic; immunosuppressive; antimicrobial; therapy; cell proliferation; treatment; cell differentiation; cancer; immune disease; rheumatologic disease; transplant rejection; anti-infective; CR6; ss.
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                                                                                                                                                                                    Example IV;
                                                                                                                                                                                                                         polypeptide
                                                                                                                                                                                                                           Novel antibody or antibody fragment which selectively binds polypeptide encoded by cytokine response gene 2.
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P-PSDB; AAY87957.
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93US-00104736.
94US-00330108.
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Best Local Similarity
Matches 542; Conserv
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                                                                                                Нопо
                                                               CDS
                                                                                                                     degenerative
                                                                                                                                            Human;
                                                                                                                                                                Human SYG972 gene coding sequence
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                                                                                                                               cancer;
                                                                                                                                SYG972; cancer diagnosis; cell differentiation; cytostatic; cancer; lymphoma; Alzheimer's disease; Parkinson's disease;
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30-DEC-1998;
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98KR-00063958.
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cc patient sample containing mRNA, analysing gene expression using the mRNA characteristics in a gene expression signature of the mRNA, and using that results in a gene expression signature to diagnose or analyse the autoimmune disease cor arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention contributer comprises: a treatment of the gene signature. The invention of genes for targeting in the treatment of rheumatoid arthritis; identification of context than a mouse; diagnosis of rheumatoid arthritis in a mammal context of genes chip, specific for rheumatoid arthritis; diagnosis or canalyses of autoimmune disease or rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collagentinduced arthritis; and reducing the symptoms associated with collagentinduced arthritis. The compositions of the invention have the following activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic, antigout, antiinflammatory, dermatological, and immunomodulatory. The methods and compositions of the present invention have the following contended arthritis, lupus, antylosing spondylitis, fibrositis, contended arthritis, gout, juvenile riheumatoid arthritis, and an immune disease caused by an infectious agent. This polynucleotide contended arthritis, and an infectious agent. This polynucleotide contended arthritis and contended arthritis contended arthritis and contended arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyaigia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hirsch R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease; arthritide; gene expression analysis; rheumatoid arthritis; collagen induced; immunempressive; antirheumaticantiarthritic; osteopathic; antigout; antiinflammatory; dermatological; immunemodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP65476 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a
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                                                                 Human; c-Jun-N- terminal kinase pathway; JNK pathway; cytostatic; programmed cell death; TNFalpha; Fas; TRAIL; genotoxic agent; cance apoptosis; Gadd45beta; JNKK2; chronic inflammatory disease; Gadd45; autoimmune condition; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1066 BP; 199 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for modulating pathways leading to programmed cell death, comprising selecting a target within the c-Jun-
CC terminal kinase (JNK) pathway, and interfering with the target using CC an agent that either up regulates or down regulates the JNK pathway. The method of the invention has cytostatic activity. A method of the CC invention is useful for modulating pathways leading to programmed cell CC death induced by TNRalpha, Fas, TRAIL, genotoxic agent such as CC deunorubicin or cisplatinum. Another method of the invention is useful CC for screening and identifying an agent, preferably peptides, peptide CC enimetrics, peptide-like molecules, mutant proteins, CDNAs, antisense CC oligonucleotides or constructs, lipids, carbohydrates or synthetic or natural chemical compounds, that modulate JNK pathway in vitro. A method of the invention may also be useful for treating cancer, and for preventing apoptosis. Compounds that are capable of interfering with the CC ability of Gadd45beta to associate with JNKK2 are useful for treating cand certain types of cancer. The present sequence is used in the
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Best Local Similarity
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12-OCT-2001; 2001US-0328811P.
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The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; diagnosis or analyses of acondidate drug in vitro for the treatment of collagen-induced arthritis; and reducing the symptoms associated with collagen-induced arthritis. The compositions of the invention have the following activities: immunosuppressive, antirheumatoi, antiarthritic, osteopathic, antigout, antiinflammatory, dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease or arthritis, and an immune disease caused as an infectious agent whis nolvinitis, and an immune disease caused as an infectious agent whis nolvinitatis, and an immune disease caused as an infectious agent whis nolvinitatis, and an immune disease.
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03-MAR-2004. EP1394274-A2

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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) a morthial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (5) a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the gene through an RNAi effect or an antibody recognising a probe has been immobilised to assay a marker gene. (I) has respiratory and antisathma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (I) has respiratory and antisathma or chronic obstructive pulmonary disease. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present
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100.0%; Pred. No. 5.8e-113;
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Query Match
Best Local Similarity
Matches 542; Conserv

Conservative

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Mismatches

Sequence 1078 BP; 200 A; 297 C; 382 G; 199 T; 0 U; 0 Other;

98.4%; Score 542; DB 13; 100.0%; Pred. No. 5.8e-113;

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                                                     The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Classifying a breast cancer patient according to prognosis determining the similarity between the level of expression five genes in a cell sample taken from patient, to control
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Cell death; apoptosis; degeneration; cancer; cytostatic; neoplasm; immunotherapy; chemotherapy; gene therapy; gadd45; Jun N terminal kinase modulator; gene; ds.
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Best Local Similarity
Matches 542; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to methods and compositions for modulating pathways leading to programmed cell death or apoptosis. The method involves selecting a target within the c-Jun-N-terminal kinase (JNK) pathway and interfering the target by an agent that either upregulates or downregulates the JNK pathway. The JNK modulator is effective in treating degenerative disease and cancer. The method and compositions of the invention are useful in immunotherapy, cancer chemotherapy and in gene therapy. The present sequence is the human gadd45 DNA which is a modulator of JNK pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for modulating pathways leading to programmed cell death for treating cancer, by obtaining peptide having specific amino acid sequent and regulating JNK pathway using peptide or composition developed using peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1078 BP;
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AAT74048 ID AAT74048 standard; XX

CDNA; 1036

RESULT 11

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cDNA clone GEN-554H06, which includes a separately claimed coding region (see AAT74047), corresponds to a novel gene, designated as human GRP17 (Gadd45 and MyD118 related protein, 17 kDa), that is associated with arrest of cell growth and DNA damage induction. It encodes a protein (see AAW23533) that is highly homologous to proteins encoded by gadd45 and MyD118 genes, both of which are tumour suppressors. The gene maps to chromosome 9922.1-22.2 GEN-55H06 was isolated from a human placental cDNA library on the basis of homology with gadd45 and MyD118. It is thought that the gene, when it is abnormal, may possibly induce cancer or malformation, and that it may be applied clinically in the diagnosis and/or treatment of cancer, malformation and autoimmune diseases, as well as for screening drugs for treatment of these conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                               ery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New GRP17 gene associated with arrest of cell growth and induction damage - useful for diagnosis and treatment of cancer, auto-immune diseases etc., also for drug screening.
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                         AATGTGACCTTCTGTGTGCTGCGGCTGCGGGTGAGGAGGACGAGGGCGACATCGCGCTGCAG 240
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The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes, detecting the hybridisation complexes and comparing the levels of the detected
                                                                                                                                                                                                                                                                                                                                                 A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
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                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 820; 50pp; English.
                                                                                                                                                                                                                                                                                                                         or osteoarthritis.
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hybridisation complexes with the level of hybridisation complexes detected in a non-diseased sample, where an altered level of the detected hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a method for identifying a plurality of polynucleotide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of immunopathology, such as Crohn's disease, asthma, ulcerative colitis, hypereosinophilia, irritable bowel syndrome, osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in identifying agents for the treatment of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of mRNAs, cDNAs or genomic fragments. This sequence represents a human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html.
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 540; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to polynucleotides which are used as probes to detect genes differentially expressed in an immunological response, abundantly expressed in an immunological response and/or coding for a polypeptide known to regulate blood cell biology. The polynucleotides are useful in research and diagnostic applications particularly in cancer and immunopathological conditions, such as AIDS, allergies, anaemia, asthma, atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple sclerosis, osteoporosis, pancreatitis, infections and arthritis. The present sequence represents a human lymph node cDNA used to detect blood cell and immunological response gene expression. Note: The present sequence does not appear in the printed specification but was obtained in electronic format from the USPTO web site (seqdata.uspto.gov/sequence.html?DocID=20040077003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New compositions having a number of first, second and third polynucleotide probes, useful in research and diagnostic applications cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; gene; human; immunological response; blood cell; cancer; immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis; bronchitis; ulcerative colitis; diabetes; multiple sclerosis; osteoporosis; pancreatitis; infection; arthritis; lymph node.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 750 BP; 120 A; 218 C; 280 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15;
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                                                    ATCCATTTTACGCTGATCCAGGCTTTCTGCTGCGAGAACGACATAGTGCACATAGTGCGCGTG
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                                 ATCCATTTACGCTGATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTG
                                                                                                       AATGTGACCTTCTGTGTGCTGCTGCGGGTGAGGAGGACGACGGGGGGACATCGCGCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stuart SG,
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 527.8; DB 13; Pred. No. 9e-110; 0; Mismatches 2;
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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        Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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Example 2; SEQ ID NO 7602; 210pp; English.

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cyrostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

Sequence 1202 BP; 226 A; 314 C; 416 G; 220 T; 0 U; 26 Other;

ches 514; Conservative ry Match Local Similarity 682 622 562 361 502 301 442 241 ATCCATTTTACGCTGATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTG 382 181 322 262 NNNNNAGGNTGCAGGGTGCCGGGAAAGCGCTGCATGAGTTGCTGCTGTCGGCGCAGCGT 202 541 481 421 121 742 61 ACAGCCAGGATGCAGGGTGCCGGGGAAAGCGCTGCATGAGTTGCTGCTGCTGTCGGCGCAGCGT 1 CTGGTTGATCGCACTATGACTCTGGAAGAAGTCCGCGGCCAGGACACAGTTCCGGAAAGC CAGGGCTGCCTCACTGCCGGCGTCTACGAGTCAGCCAAAGTCTTGAACGTGGACCCCGAC 8 ACCCTCCCCGAGTGACAGCCCCGGCGGGACCTTCGTCTGATCGACCTGGTGACGCCCCGG 540 GAGAAGCTCAGCCTGTTTTGCGAGGAGAGAGCCGCAGCGTTAACGACTGGGTGCCCAGCATC GACCTGCACTGCATCCTCATTTCGAACCCCCAACGAGGACGCCTGGAAGGATCCCGCCTTG GGCGATGTGCAGCGGCTGGCGGCTATCGTGGGCGCCGAGGAGGCGGGGTGCGCCGGGC AATGTGACCTTCTGTGTGCTGCCTGCGGGTGAGGACGACGACGACGACATCGCGCTGCAG ନ ACCCTCCCGAGTGACAGCCCGGCGGGGACCTTGGTCTGATCGACGTGGTGACGCCCCGG GAGAAGCTCAGCCTGTTTTGCGAGGAGAGCCGCAGCGTTAACGACTGGGTGCCCAGCATC GACCTGCACTGCATCCTCATTTCGAACCCCCAACGAGGACGCCTGGAAGGATCCCGCCTTG GCGATGTGCAGCGGCTGGCGGCTATCGTGGGCGCCGGCGAGGAGGCGGGTGCGCCCGGGC ATCCATTTTACGCTGATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTG AATGTGACCTTCTGTGTGCTGGCTGCGGGTGAGGAGGACGAGGGCGACATCGCGCTGCAG CAGGGCTGCCTCACTGCCGGCGTCTACGAGTCAGCCAAAGTCTTGAACGTGGACCCCGAC 542 743 93.1%; 0; Mismatches Score 512.8; DB 12; Length 1202; Pred. No. 2.4e-106; Indels 0, Gaps 60 741 681 480 621 420 561 360 501 300 441 240 381 180 321 120

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                                                                                                   gb_est1: *
gb_est4: *
gb_est5: *
gb_est6: *
gb_htc: *
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

FEATURES source		TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BU074910 LOCUS DEFINITION
(hinoue@im.wustl.edu) (Seq primer: -40RP from Gibco High quality sequence stop: 448. Location/Qualifiers 1. 596 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"	MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Library was constructed by Crypten University Genome Sequencing Center For information on Obtaining a clone please contact: Dr. Hiroshi Inoue	Endocrine Pancreas Consortium Unpublished (2000) Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,		BU074910 BU074910.1 GI:22516099 EST. Homo sapiens (human) Homo sapiens	BU074910 596 bp mRNA linear EST 27-AUG-2002 im78c11.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6041108 5' similar to SW:G45G HUMAN 095257 GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45 GAMMA ;, mRNA sequence.

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Mammalia; Eutheria;
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                                                                              Homo sapiens (human)
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/tissue_type="Purified pancreatic islet"
/lab_host="pH108"
/clone_lib="HR85_islet"
/clone_lib="HR85_islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site_2: Xho1; CDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5',
Xho1 site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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1 (bases 1 to 637)

1 (bases 1 to 637)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Melton, D., Brown, J., Kenty, G., Gradwohl, G., Clifton, S., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Schmitt, A., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
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MA 02138
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Other ESTS: ip14N09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information
obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 617-495-1812
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Seq primer: -40RP from Gibco
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/clone lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site_2: Kho1; CDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
Xho1 site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:6217576"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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National Institutes of Health, Mammalian
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quality sequence stop: 661.
Location/Qualifiers
                                                                                                                                                                                                                  98.4%; Score 542; DB 2; Local Larity 100.0%; Pred. No. 7.5e-120; Conservative 0; Mismatches 0;
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="TMAGE:5222346"
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/note=Torgan: pooled pancreas and spleen; Vector:
/note=Torgan: pooled pancreas and spleen; Vector:
/note=Torgan: pooled pancreas and pancreas from 28 yo
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size: 15 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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National Institutes of Health, Mammalian Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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       /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clome="IMAGE:3528409"
/clome="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/lone 11b="NIH MGC 17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
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information can be at: image.llnl.gov

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Hominidae; Homo.

1 (bases 1 to 730)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                  BE795063
BE795063.1 GI:10216261
EST.
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601592875F1 NIH_MGC_7 Homo
mRNA sequence.
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini
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cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM807 row: f column: 20
High quality sequence stop: 730.
Location/Qualifiers
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/tissue_type="small_cell_carcinoma"
/tell_line="MGC3"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/clone="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/core:"Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: Notation: pOTB7; Site_2: Notati
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/db_xref="taxon:9606"
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542; Conser
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Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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CR605667.1 GI:50486474
HTC; CNSLT_CDNA.
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1 (bases 1 to 1031)
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2 (bases 1 to 1031)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                GACCTGCACTGCATCCTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTG
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               GACCTGCACTGCATTCCCAACCCAACGAGGACGCCTGGAAGGATCCCGCCTTG
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDDI049YE24"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Best Local Similarity
Matches 542; Conserv
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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HTC; CNSLT_cDNA.
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Location/Qualifiers
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                                                             CTGGTTGATCGCACTATGACTCTGGAAGAAGTCCGCGGCCAGGACACAGTTCCGGAAAGC
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                                                                                                                                                                                                                                                      98.4%; Scilarity 100.0%; P
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/tissue_type="Placenta
/plasmid="pCMVSPORT_6"
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/db_xref="taxon:9606"
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Pred. No. 7.8e-120;
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1 (bases 1 to 1049)

1i,W.B., Gruber,C., Jessee,J

Full-length cDNA libraries a:
Unpublished

Contact: Feng Liang Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        full-length cDNA clone CS0DI084YK05 of Homo sapiens (human). CR619521 GI:50500328 HTC; CNSLT_CDNA.
                                                                                                                                                                                                                                                                                         division of Invitrogen.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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CTGGTTGATCGCACTATGACTCTGGAAGAAGTCCGCGGCCAGGACACAGTTCCGGAAAGC
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                                                            Conservative
                                                                                                                                                  /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="CSDDI084YK05"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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                                                      lst strand cDNA was primed with a NotI-Oligo(GI) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                      Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                    Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation Faraday Avenue 2 (bases 1 to 1052)
                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                       Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                        Location/Qualifiers
      /organism="Homo sapiens"
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CR591382.1 GI:50472189
HTC; CNSLT ONE
Hominidae; Homo.

1 (bases 1 to 1062)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ InVitroGen Corporation

Faraday Avenue
2 (bases 1 to 1062)
                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/db_xref="taxon:9606"
/clone="CSODIO34YP19"
/tissue_type="Placenta_C
/plasmid="pCMVSPORT_6"
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TITLE
JOURNAL
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Best Local Similarity
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Direct Submission

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr |

- Web : www.genoscope.cns.fr |

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMV5PORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CSODIO34YD21"
/tissue_type="placenta Cot 2:
/plasmid="pCMVSPORT_6"
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71 60129929F1 NIH_MGC_7 Homo mRNA sequence. BF219948 BF219948.1 GI:11126042

sapiens

mRNA linear EST 08-NOV-2000 cDNA clone IMAGE:2822765 5',

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High quality sequence stop: 678.
Location/Qualifiers
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Homo sapiens
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Plate: IRAL1 row: j
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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1 (bases 1 to 718)
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Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/clone lib="NIH_MGC_7"
/clone="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/cell_line="MGC3"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822765"
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Pred. No. 1.4e-118;
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JOURNAL COMMENT
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AUTHORS
TITLE
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Full-length cDNA libraries and normalization
Inpublished (2001)
On May 8, 2003 this sequence version replaced gi:30450722.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 1011)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                             AATGTGACCTTCTGTGTGCTGGCTGCGGGTGAGGACGAGGGCGAGGGCGACATCGCGCTGCAG
                                                                                                                                               CAGGGCTGCCTWACTGCCGGCGTCTACGAGTCAGCCAAAGTCTTGWACGTGGACCCCGAC
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/db_xref="taxon:9606"
/clone="CSODIO29YO17"
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Pred. No. 2.8e-117;
4; Mismatches 6;
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BI117459.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 774)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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602867522F1 NIH_MGC_7 Homo
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/lab host="DHIOB (phage-resistant)"
/clone lib="NIH MGC 7"
/clone=Torgan: lung; Vector: pOTB7; Site 1: XhoI; Site_2:
RocRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                         /clone="IMAGE:5016316"
/tissue_type="small cell
/cell_line="MGC3"
                                                                                                                                                                                                                                                                        mol_type="mRNA"
db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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Best Local Similarity
Matches 542; Conserv
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VCE 1 (M.B., Gruber, C., Jessee, J. and Polayes, D.

RI, W.B., Gruber, C., Jessee, J. and Polayes, D.

Rull-length cDNA libraries and normalization

Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30609433.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster

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                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.4e-117;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                         sapiens (human)
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Idomo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Idomo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          information about this cluster, see
www.genoscope.cns.fr/cdna?s=CSODIO34CB11QP1&c=5465.f.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 7.6e-117;
1; Mismatches 0;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11610 row: a column: 19
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 594)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                              GGAGAAGCTCAGCCTGTTTTGCGAGGAGAGCCGCAGCATTAACGACTGGGTGCCCAGCAT
                                                                                                                              CGACCTGCACTGCATCCTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTT
                                                                                                                                                                                       GGGCGATGTGCAGCGGCTGGCGGCTATCGTGGGCGCCGGCGAGGAGGCGGGTGCGCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
/clone lib="NHH MGC 121"
/site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is obligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5241882"
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Pred. No. 8.1e-117;
0; Mismatches 1;
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Length Indels

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sequence 13536, A
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 2210, Ap
Sequence 2210, Ap
Sequence 3524, Appl
Sequence 902, App
Sequence 9170, Ap
Sequence 9170, Ap
Sequence 91111, Ap
Sequence 1111, Ap
Sequence 11167, A

Sequence Sequence Sequence

11, Appl 11, Appl 61825, A 13536, A 1132, Ap

Sequence Sequence Sequence Sequence

1, Appli 2368, Ap 1, Appli 59, Appl

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l number of hits satisfying chosen parameters:
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1: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/BCOMB.seq:*
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         2 US-08-463-081B-11

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3 US-08-465-3873

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3 US-09-879-833-1

2 US-08-797-831A-3

2 US-08-463-081B-31

2 US-08-463-390B-31

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US-08-463-081B-11
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Patent No. 5871960
Patent No. 5871960 5837487
GENERAL INFORMATION: Rendall A. & Beadling, Carol
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
                                                                                                                                           APPLICATION NUMBER: US/08/463,081B
APPLICATION DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILLING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILLING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGREROCE/DOCKET NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 966 38150
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                       TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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ADDRESSEE: PRETTY, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 444 South
CITY: Los Angeles
STATE: California
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US-09-880-107-2368
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US-08-330-108-11
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US-09-949-016-13536
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Score

Match

Query

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FEATURE:
NAME/KEY:
LOCATION:
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ches 542;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
                                                                                                                                                                                                                   APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide, TITLE OF INVENTION: Vector and Transformed Cell Thereof, and TITLE OF INVENTION: Expression Thereof NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           |uence 11, Application US/08461379A
|ent No. 5871961
|WERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   -461-379A-11
                                                                                                         ADDRESSEE: Ratner & Prestia
ADDRESSEE: (B) STREET:One Westlakes-Berwyn
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
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APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: WSSN 08/330,108; 08/104,736
APPLICATION NUMBER: & 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amze1, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: (610)470-0701
TELEPAX: (610)470-0701
TELEPAX: 11:
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98..575
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100.0%; Pr
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RESULT 3 US-08-462-390B-11

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APPLICATION NUMBER: USSN 08/330,108
APPLICATION NUMBER: USSN 08/104,736
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quence 11, Application US/08462390B
Lent No. 5882894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (610)407-0701
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ches 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/462,390B
FILING DATE: 5-UNE-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: cDNA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1065 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Valley Forge
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ADDRESSEE: . (B) STI
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GGCGATGTGCAGCGGCTGGCGGCTATCGTGGGCGCCGGCGAGGAGGCGGGGTGCGCCGGGC 360
                                                                                                                                                                                                                    CAGGGCTGCCTCACTGCCGGCGTCTACGAGTCAGCCAAAGTCTTGAACGTGGACCCCGAC
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                                                              ATCCATTTTACGCTGATCCAGGCTTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTG
                                                                                                                              AATGTGACCTTCTGTGTGCTGGCTGCGGGTGAGGAGGACGAGGGCGACATCGCGCTGCAG
                                                                                                                                                                                                                                                                                                       ACAGCCAGGATGCAGGGTGCCGGGAAAGCGCTGCATGAGTTGCTGCTGTCGGCGCAGCGT 202
                                           ATCCATTTTACGCTGATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTG
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(610)407-0701
'OR SEQ ID NO: 11:
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                                                                          US-08-463-074B-11
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GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 542; Conserva
                                                                                                                                                                                                                                                                        FILING DATE: 5-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/104,736

FILING DATE: 10-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/796,066

FILING DATE: 20-NOV-91

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel, Ph. D.

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)

TELEPHONE: (213) 622-7700

TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074
                                                                                                                                                                                                                                            TELEFAX: (213) 489-42: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pair
                                                                                                                             FEATURE:
                                                                                                                                             MOLECULE TYPE:
                                                                                         NAME/KEY:
LOCATION:
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STATE: California
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                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                         LENGTH: 1065 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                            (213) 489-4210
        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0,
                                                                                           98..575
                                                                                                                                                             linear
       98.4%; Score 542; DB 3; L
100.0%; Pred. No. 1.9e-115;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/463,074B
                                          Length 1065;
            Indels
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              Gaps
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PILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                puence 11, Application US/08465585C ent No. 6027914
RERAL INFORMATION:
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-465-585C-11
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6
TITLE OF INVENTION: Transformed Cell Thereof, a
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: PRETTY, SO
ADDRESSEE:
CITY: Los Angeles
STATE: Californiaa
                                                                                                                                                                                                                     APPLICATION NUMBER:
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(B) STREET:
20-NOV-1991
INFORMATION:
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RESULT 6
US-08-652-446-11
Sequence 11, Application US/08652446
Sequence 11, Application US/08652446
Patent No. 6057427
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carolination of Invention: Nucleic Acids Encoding CR.
TITLE OF INVENTION: Expression Thereof
INVENTION: Expression Thereof
NUMBER OF SEQUENCES: 38
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REFERENCE/DOCKET NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 622-7700
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TENGTH: 1065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local S
Matches 542
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NAME/KEY:
LOCATION:
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APPLICATION NUMBER: 08/465,585
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION UNBER: 08/461,379
PRIOR APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
APILICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/ACENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
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FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
OR/463.074
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SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compactible
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: 1
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CITY: Los Angeles
STATE: California
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR RETLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEG ID NO 3873

LENGTH: 1065

TYPE: DNA
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US-09-49-016-3873
; Sequence 3873, Application US/09949016
; Patent NO. 6812339
; Patent NO. 6812339
; Patent NO. 6812339
; FARMATION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTIC
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| LERAL INFORMATION:
| PAICANT: Park, Chong-Hun; SAMYANG GENEX CORPORATION
| PLICANT: Park, Chong-Hun; SAMYANG GENEX CORPORATION
| TLE OF INVENTION: CANCER DIAGNOSIS METHOD USING CELL GROWTH INHIBITING AND CELL DIF
| TLE OF INVENTION: FERENTIATION SPECIFIC SYG972 GENE AND GENOMIC DNA AND PROMOTER TO THE OF INVENTION: BREOF
| LE REFERENCE: PA/SYG/99601 |
| IRRENT APPLICATION NUMBER: US/09/879,833 |
| IRRENT FILING DATE: 1901-106-12 |
| IOR APPLICATION NUMBER: KR 54933 |
| IOR FILING DATE: 1998-12-12 |
| IOR APPLICATION NUMBER: KR 63958 |
| IOR FILING DATE: 1998-12-30 |
| IMBED OF GENT IN NOC. 3
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RGANISM: HL60 cell line
R79-833-1
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)FTWARE: KOPATIN 1.5
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                                                                                            ACAGCCAGGATGCAGGGTGCCGGGAAAGCGCTGCATGAGTTGCTGCTGTCGGCGCAGCGT
                                                                                                                                                                                                                                                98.4%; Score 542; DB 3; Length 1066; 100.0%; Pred. No. 1.9e-115; tive 0; Mismatches 0; Indels
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US-08-797-831A-3
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                                                                        TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGINAL SOURCE:
ORGANISM: Human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08797831A Patent No. 5808031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Miklo, SUZUKI
APPLICANT: Takeshi, WATANABE
APPLICANT: TSutomu, FUJIWARA
TITLE OF INVENTION: GRP17 GENE
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CLONE: GEN-554H06C
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7860
TELEPAX: (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patent In Release #1.24 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion,
                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/797,831A FILING DATE:
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CITY: Washington
COUNTRY: United States
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2100 Pennsylvania Avenue, N.W.
                                                                        Human placenta cDNA library
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:puence 820, Application US/09023655
Lent No. 6607879
ENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DET
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS: 1508
CORRESPONDENCE ADDRESS: INC.
STREEF: 174 NORTED DETVE
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            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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 US/09/023,655
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Pred. No. 1.1e-114;
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ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0.
TELEPHONE: (650) 85-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 820:
SEQUENCE CHARACTERISTICS:
LENGTH: 750 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.8%;
Best Local Similarity 99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE:
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CLONE: 828764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTGGTTGATCGCACTATGACTCTGGAAGAAGTCCGCGGCCAGGACACAGTTCCGGAAAGC
                                                                                                                                                                                             GACCTGCACTGCATCCTCATTTCGAACCCCAACGAGGACGCCT-GGAAGGATCCCGCCTT
                                                                                                                                                                                                                                       GGCGATGTGCAGCGGCTGGCGGCTATCGTGGGCGCCGGCGAGGAGGAGGCGGGTGCGCCCGGGC 360
                                                                                                                                                                                                                                                                                               ATCCATTTTACGCTGATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTG
                                                                                                                                                                                                                                                                                                                   ATCCATTTTACGCTGATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTG
                                                                                                                                                                                                                                                                                                                                                        AATGTGACCTTCTGTGTGCTGGCTGCGGGTGAGGAGGACGAGGGGGACATCGCGCTGCAG
                                                                                                                                                                                                                                                                                                                                                                          AATGTGACCTTCTGTGTGCTGGCTGCGGGTGAGGACGACGACGACGACATCGCGCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGTTGATCGCACTATGACTCTGGAAGAAGTCCGCGGCCAGGACACAGTTCCGGAAAGC
                             GGG 542
                                                                                                                                     GGAGAAGCTCAGCCTGTTTTGCGAGGAGAGCCGCAGCGTTAACGACTGGGTGCCCAGCAT 479
                                                                                                                                                                            GACCTGCACTGCATCCTCATTTCGAACCCCAACGAGGACGCCTGGGAAGGATCCCGCCTT
                                                                                  CACCCTCCCGAGTGACAGCCCGGCGGGGACCTTGGTCTGATCGACGTGGTGACGCCCCG 539
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ନୁନ
                                                           CACCCTCCCCGAGI
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RESULT 11 US-08-463-081B-31 ; Sequence 31, Application US/08463081B ; Patent No. 5871960

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PRICALLOW NUMBER: US 08/00/103/0015

PRIOR APPLICATION DATA,
APPLICATION NUMBER: US 08/104,736

FILING DATE: 10-AUG-1993

PRIOR APPLICATION NUMBER: US 07/796,066

FILING DATE: 20-NOV-91

APPLICATION NUMBER: US 07/796,066

FILING DATE: 20-NOV-91

ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, ph. D.
REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700

TELEPHONE: (213) 489-4210

IFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 base pairs

TYPE: nucleic acid
CTPANITONERS: Cincil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 1i:
MOLECULE TYPE:
4-463-081B-31
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TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,081B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ches 477; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 444 South Flower St. - Suite 1900 CITY: Los Angeles STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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376 CTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTGGAGAAGCTCAGCCTG 435
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                                                                                                                                                                                                                                        GTGCTGGCTGCGGGTGAGGAGGACGAGGGCGACATCGCGCTGCAGATCCATTTTACGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGCGGCTATCGTGGGCGCCGGCGAGGAGGCGGGCGGGTGCCGCCGGGCGACTGCACT 375
                                                                                                                              ATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTGGGCGATGTGCAGCGG
                                                                                                                                                      ATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTGGGCGATGTGCAGCGG 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.6%; Score 477; DB 2; Length 477; 100.0%; Pred. No. 1.5e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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рb	361 CTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTGGAGAAGCTCAGCCTG 420
8	436 TTTTGCGAGGAGAGCCGCAGCGTTAACGACTGGGTGCCCAGCATCACCCTCCCCGAG 492
ф	421 TTTGCGAGGAGACCGCAGCGTTAACGACTGGGTGCCCAGCATCACCCTCCCCGAG 477
RESULT	T 12 461-779A-31
; Sequence ; Patent No.	Lence 31. Application US/08461379A ent No. 5871961
GEN	INFORMATION:
·· ··	OF INVENTION: Nucleic Acids Encoding CR5 Polypeptid
	DF INVENTION: Vector and Transformed Cell Thereof DF INVENTION: Expression Thereof
	OF SEQUENCE
·· ··	SSEE: Rati
	SSEE: . (B) S
•• ••	STATE: Pennsylvania
• ••	_ R
	COMPUTER READABLE FORM:
	JTER: IBM PC compatible
~- ~-	SOFTWARE: PatentIn Release #1.0,
	NARE: VEISION #1.25
·· ··	FILING DATE: 5-JUNE-1995
٠. ٠.	ICATION NUMBER:
	APPLICATION NUMBER: & 07/796,066 FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
	<pre>EY/AGENT INFORMA : Viviana Amzel</pre>
	STRATION NUMBER: 30,5
٠. ٠. ٠	MUNICATION INFORMATION: PHONE: (610)470-0700
 INI	TELEFAX: (610)470-0701 FORMATION FOR SEO ID NO: 31:
	CE CHARACTERISTICS:
·· ··	TYPE: nucleic acid
٠. ٠.	S E
us-08-	MOLECULE TYPE: cDNA -461-379A-31
Query N Best Lo Matches	ry Match 86.6%; Score 477; DB 2; Length 477; t Local Similarity 100.0%; Pred. No. 1.5e-100; ches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
δ	16 ATGACTCTGGAAGAAGTCCGCGGCCAGGACACAGTTCCGGAAAGCACAGCCAGGATGCAG 75
Db	1 ATGACTCTGGAAGAAGTCCGCGGCCAGGACACAGTTCCGGAAAGCACAGCCAGGATGCAG 60
Qγ	76 GGTGCCGGGAAAGCGCTGCATGACTTGCTGCTGTCGGCGCAGCGTCAGGGCTGCCTCACT 135
Db	61 GGTGCCGGGAAAGCGCTGCATGAGTTGCTGTCGGCGCAGCGTCAGGGCTGCCTCACT 120
Ş	136 GCCGGCGTCTACGAGTCAGCCAAAGTCTTGAACGTGGACCCCGGACAATGTGACCTTCTGT 195
Db	121 GCCGGCGTCTACGAGTCAGCCAAAGTCTTGAACGTGGACCCCCGACAATGTGACCTTCTGT 180
Ş	196 GTGCTGGCTGCGGGTGAGGAGGACGAGGCGACATCGCGCTGCAGATCCATTTTACGCTG 255
문	181 GTGCTGCGGGTGAGGAGGACGACGACATCGCGCTGCAGATCCATTTTACGCTG 240

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versi:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 477 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                             1:ches
                                                                                                                ery Match
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ent No. 5882894
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                                                                                                                                                          8-462-390B-31
                                                                                                                                                                                                                                                                                                TELEFAX: (610)407-0701 FORMATION FOR SEQ ID NO:
                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Pennand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                Local Similarity
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                                 16 ATGACTCTGGAAGAAGTCCGCGGCCAGGACACAGTTCCCGGAAAGCACAGCCAGGATGCAG
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Pennsylvania
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                                                                             Conservative
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                                                                    86.6%; 5c.
100.0%; Pr/
0;
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                                                                                                                                                                                                                                                                                                  31:
                                                                             Score 477; DB 2; Lo
; Pred. No. 1.5e-100;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:One Westlakes-Berwyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version
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                                                                                                                Length 477
                                                                               Indels
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US-08-463-074B-31
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                                                                                                                                   APPLICATION NUMBER: US 07/796
APPLICATION UNBER: US 07/796
FILING DATE: 20 NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: VIVIANA Anzel, Ph. D.
REGISTRATION NUMBER: 966
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                      TELEFAX: (213) 489-421 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Smith, Kendall A. & Beadling, Ca
TITLE OF INVENTION: Nucleic Acids Encoding
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/463,0741
FILING DATE: 5-JUN-1995
PRIOR APPLICATION UDATA:
APPLICATION UNBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
                                               LENGTH: 477 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376
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(B) STREET:
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APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUNE 1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Anzel, ph. D.
REGISTRATION NUMBER: 30,930
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APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6
TITLE OF INVENTION: Transformed Cell Thereof,
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      puence 31, Application US/08465585C
ent No. 6027914
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-465-585C-31
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STATE: Californiaa
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(B) STREET:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 477;
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421
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Similarity 100.0%; Pred. No. 1.5e-100;
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                               TTTTGCGAGGAGAGCCGCAGCGTTAACGACTGGGTGCCCAGCATCACCCTCCCCGAG
                                                           CTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTGGAGAAAGCTCAGCCTG
                                                                               CTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTGGAGAAGCTCAGCCTG
                                                                                                                           ATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTGGGCGATGTGCAGCGG
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Search completed: June 4, 2006, 22:37:55 Job time: 176 secs

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/EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq: *

/EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq: *

/EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq: *

/EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq: *

/EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq: *

/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq: *

/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq: *
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Match
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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6 US-10-287-436A-712
10 US-10-263-330-9
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10 US-10-264-985-736
10 US-10-278-698-736
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10 US-10-287-436A-86
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10 US-10-631-643-80
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Sequence 275, App
Sequence 1, Appli
Sequence 712, App
Sequence 9, Appli
Sequence 1310, Ap
Sequence 1310, Ap
Sequence 9, Appli
Sequence 221, App
Sequence 736, App
Sequence 37, Appl
Sequence 820, App
Sequence 3639, Ap
Sequence 7602, Ap
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT FILING DATE: 2004-04-07
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 275
SEQ ID NO 275
SEQ ID NO 275
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                                                                                                                                                                                                                                                                                                        Matches 542; Conservative
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AATGTGACCTTCTGTGTGCTGGCTGCGGGTGAGGACGACGACGACGACATCGCGCTGCAG
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ILE REFERENCE: PA/SYG/99601

RRENT APPLICATION NUMBER: US/09/879,833

RRENT FILING DATE: 2001-06-12

!IOR APPLICATION NUMBER: KR 54933
!IOR FILING DATE: 1998-12-12
!IOR APPLICATION NUMBER: KR 63958
!IOR FILING DATE: 1998-12-30

NBER OF SEQ ID NOS: 3

PTWARE: KOPATIN 1.5

) ID NO 1

ENGTH: 1066
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TILE OF INVENTION: CANCER DIAGNOSIS METHOD USING CELL GROWTH INHIBITING AND CELL DITTLE OF INVENTION: FERENTIATION SPECIFIC SYG972 GENE AND GENOMIC DNA AND PROMOTER TILE OF INVENTION: EREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    puence 1, Application US/09879833
ent No. US20020055107A1
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RGANISM: HL60 cell line
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                                                        AATGTGACCTTCTGTGTGCTGGCTGCGGGTGAGGAGGACGAGGGCGACATCGCGCTGCAG
                                                                                        AATGTGACCTTCTGTGTGCTGGCTGCGGGTGAGGAGGACGAGGGCGACATCGCGCTGCAG
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100.0%; Pred. No. 4.5e-150;
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; Publication No. US20050202421A1

; GENERAL INFORMATION:
APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
ITILE OF INVENTION: METHOD FOR DIAGNOSIS AND TRE
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TRE
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TRE
; TITLE OF INVENTION: METHOD ARTHRITIS
; FILE REFERENCE: 10872.514696

; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 712
; SEQ ID NO 712
; LENGTH: 1066
TYPE: DNA
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Best Local Similarity
Matches 542; Conserv
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ORGANISM: Homo sapiens
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PELICANT: FRANZOSO, GUIDO
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PELICANT: DESMAELE, ENRICO
PELICANT: ZAZZERONI, FRANCESCA
PELICANT: PAPA, SALVATORE
PELICANT: PAPA, SALVATORE
PAPA: SALVATORE
PAPA: SALVATORS OF APOPTOSIS
PAREMENT APPLICATION NUMBER: US/10/263,330
PAREMENT APPLICATION NUMBER: US/60/326,492
PRIOR APPLICATION NUMBER: US/60/326,492
PRIOR FILING DATE: 2001-10-02
PR
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DRGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 006705
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1310
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US-10-172-118-1310
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PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1310
LENGTH: 1078
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Best Local Similarity 100.0%;
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APPLICANT: Linsley, Peter
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Noberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
APPLICANT: Bernards, Rene
APPLICANT: Diagnosis and Prognosis of Breast Cancer Patients
FILE REPERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
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;; Pred. No. 4.5e-150;
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PLICANT: Roberts, Christopher J.

PLICANT: Van 't Veer, Laura Johanna
PLICANT: Van 't Veer, Marc J.

PLICANT: Van de Vijver, Marc J.

PLICANT: Bernards, Rene
TLE OF INVENTION: Diagnosis and Prognosis of
LE REFERENCE: 9301-188-99

IRRENT APPLICATION NUMBER: US/10/342,887

IRRENT FILING DATE: 2003-01-15
IOR APPLICATION NUMBER: 60/289,918
IOR APPLICATION NUMBER: 60/380,710
IOR FILING DATE: 2002-05-14
IOR FILING DATE: 2002-05-14
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PLICANT:
PLICANT:
PLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IOR APPLICATION NUMBER: 10/172,118
IOR FILING DATE: 2002-06-14
MBER OF SEQ ID NOS: 2699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   )RGANISM: Homo sapiens
)-342-887-1310
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-342-887-1310
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ENGTH: 1078
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GACCTGCACTGCATCCTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTG
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                                                                                                    GGCGATGTGCAGCGGCTGGCGGCTATCGTGGGCGCCGGCGAGGAGGCGGGTGCGCCCGGGC
                                                                                                                                          ATCCATTTTACGCTGATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTG
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He, Yudong
Linsley, Peter S.
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Roberts,
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Sequence 9, Application US/10626905
; Publication No. US20040121463A1
; GENERAL INFORMATION:
   APPLICANT: FANNZOSO, GUIDO
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: DAPA, SALVATORE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APPOPTOSIS
; FILE REFERENCE: 21459-94575
; CURRENT APPLICATION NUMBER: US/10/626,905
; CURRENT APPLICATION NUMBER: PCT/US02/31548
; PRIOR APPLICATION NUMBER: PCT/US02/31548
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR APPLICATION NUMBER: 5001-10-02
; PRIOR FILING DATE: 2001-10-02
; PRIOR PLICATION NUMBER: 60/326,492
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361 GACCTGCACTGCATCCTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTG
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                                                                                                                                                         ATCCATTTTACGCTGATCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTG
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:puence 221, Application US/10278698
inlication No. US20050037344A1
IREAL INFORMATION:
PPLICANT: PathoArray GmbH
PPLICANT: Stublmuller, Bruno
PPLICANT: Haupl, Thomas
:TILE OF INVENTION: Nucleic Acid Array
:I.E REFERENCE: 030027US
:(RRENT APPLICATION NUMBER: US/10/278,698
:(RRENT FILING DATE: 2002-10-23
:(MBER OF SEQ ID NOS: 1050
:)FTWARE: PatentIn version 3.2
) ID NO 221
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TRIGANISM: Homo sapiens
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Local Similarity 100.0%; Pred. No. 4.5e-150;
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ACCCTCCCGAGTGACAGCCCGGCGGGGACCTTGGTCTGATCGACGTGGTGACGCCCCGG
                                       GAGAAGCTCAGCCTGTTTTGCGAGGAGAGCCGCAGCGTTAACGACTGGGTGCCCAGCATC
                                                                                                               GACCTGCACTGCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTG
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Sequence 736, Application US/10278698

Publication No. US20050037344A1

GENERAL INFORMATION:
APPLICANT: PathOArray GmbH
APPLICANT: PathOArray GmbH
APPLICANT: Haupl, Thomas
TITLE OF INVENTION: Nucleic Acid Array
FILE REFERENCE: 030027US
CURRENT APPLICATION NUMBER: US/10/278,698
CURRENT FILING DATE: 2002-10-23
NUMBER OF SEQ ID NOS: 1050
SOFTWARE: Patentin version 3.2

SEQ ID NO 736
LENGTH: 1078
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; ORGANISM: Homo sapiens
US-10-278-698-736
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US-10-278-698-736
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Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 542; Conservative 0; Mismatches 0;
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GG 636
                         GG 542
                                                      ACCCTCCCGAGTGACAGCCCGGCGGGACCTTGGTCTGATCGACGTGGTGACGCCCCGG
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| UEROCE 86, Application US/10287436A
| Ileation No. US20050202421A1
| IERAL INFORMATION:
| IERAL INFORMATION:
| IERAL INFORMATION: METHOD FOR DIAGNOSIS AND TRE
| PLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
| PLICANTION: METHOD FOR DIAGNOSIS AND TRE
| TILE OF INVENTION: METHOD FOR DIAGNOSIS AND TRE
| TILE OF INVENTION: METHOD FOR DIAGNOSIS AND TRE
| LE REFERENCE: 10872.514696
| IERENT APPLICATION NUMBER: US/10/287,436A
| IRRENT FILING DATE: 2002-10-31
| IOR APPLICATION NUMBER: US 60/336,220
| IOR FILING DATE: 2001-10-31
| IOR FILING DATE: 2001-10-31
puence 37, Application US/10631467 ilication No. US20050208496A1 IERAL INFORMATION:
PLICANT: Genox Research Inc.
TLE OF INVENTION: Method for testing
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1-287-436A-86
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FTWARE: FastSEQ for Windows Version 4.0
                                                                                               1-631-467-37
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RGANISM: Homo sapiens
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Pred. No. 4.5e-150;
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     broncheal asthma,
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FILE REFERENCE: 3462.1005-000
CURRENT APPLICATION NUMBER: US/10/631,467
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR FILING DATE: 2003-03-20
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
SOFTWARE: Patentin version 3.1
SEQ ID NO 37
TENGTH. 1078
                                                                                                       RESULT 12
US-10-641-643-820
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Best Local Sim
Matches 542;
                                           Sequence 820, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1078
TYPE: DNA
ORGANISM: Homo sapiens
Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR
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GENE EXPRESSION NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:

THE DETECTION

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APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAMS: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 855-0555
TELEFAX: (650) 855-0555
TELEFAX: (650) 855-0555
TELEFAX: (550) 855-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ery Match 95.8%;
st Local Similarity 99.4%;
ches 540; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 820 :
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LIBRARY: PROSTUTO4
CLONE: 828764
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384
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STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                         GGCGATGTGCAGCGGCTGGCGGCTATCGTGGGCGCGAGGAGGAGGCGGGTGCGCCGGGC 443
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ZIP: 94304
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Pred. No. 7e-146;
0; Mismatches 2; Indels 1
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Oy 361 GACCTGG Db 446 GACCTGG Qy 421 GAGAAGG Db 506 GAGAAGG Qy 481 ACCCTGG Db 566 ACCCTGG	Db 206 CAGGGCI Qy 181 AATGTGA Db 266 AATGTGA Qy 241 ATCCATT Db 326 ATCCATT Qy 301 GGCGATC Db 386 GGCGATC	Query Match Best Local S Matches 526 Matches 61 1146	RESULT 13 US-10-723-860-3639 US-10-723-860-3639 Publication No. US2 GENERAL INFORMATION APPLICANT: Aziz, N APPLICANT: Ginsbu APPLICANT: Zlotni TITLE OF INVENTION FILE REFERENCE: 05 CURRENT FILING DATE CURRENT FILING DATE PRIOR FILING DATE: NUMBER OF SEQ ID N SOFTWARE: Patentin' SEQ ID NO 3639 LENGTH: 612 TYPE: DNA ORGANISM: Homo sa US-10-723-860-3639	6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Oy 480 CACCCTC
GACCTGCACTGCATCCCCATTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTG 420	א נא עו עו עו א	95.4%; Score 525.4; DB 9; Length 612; imilarity 99.8%; Pred. No. 3.5e-145; Conservative 0; Mismatches 1; Indels 0; Gaps 0; CTGGTTGATCGCACTATGACTCTGGAAGAAGTCCGGGCCAGGACACAGTTCCGGAAAGC 60 [RESULT 13 US-10-723-860-3639 US-10-723-860-3639 Sequence 3639, Application US/10723860 Publication No. US20040253606A1 GENERAL INFORMATION: APPLICANT: Ariz, Natasha APPLICANT: Zlotnik, Albert TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators FILE REFERENCE: 05882.0193.NPUS01 CURRENT APPLICATION UNMBER: US/10/723,860 CURRENT FILING DATE: 2003-11-26 PRIOR APPLICATION UNMBER: 60/429,739 PRIOR FILING DATE: 2002-11-26 PRIOR APPLICATION UNMBER: MODULATION SEQ ID NO 3639 SEQ ID NO 3639 LENGTH: 612 TYPE: DNA GRGANISM: Homo sapiens US-10-723-860-3639	CCCGAGTGACAGCCCGGCGGGGACCTTGGTCTGATCGACGTGGTGACGCCCCG	ccccaAcreAcAcccccccccacacAccrrccrrccaAccarcaAccaccaccccc 539

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EATURE:

HAME/KEY: misc feature

CATION: (243)..(267)

THER INFORMATION: n is a

EATURE:
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PLICANT: Aziz, Natasha
PLICANT: Aziz, Natasha
PLICANT: Zlotnik, Albert
TLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
TLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
REFERENCE: 05882.0193.NPUSO!
RRENT APPLICATION NUMBER: US/10/723,860
RRENT FILING DATE: 2003-11-26
IOR APPLICATION NUMBER: 60/429,739
IOR FILING DATE: 2002-11-26
IMBER OF SEQ ID NOS: 8393
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OCATION: (271)...(271)
THER INFORMATION: n is
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t Local Similarity
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                                                                        ACCCTCCCGAGTGACAGCCCGGGGGGACCTTGGTCTGATCGACGTGGTGACGCCCCGG
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Pred. No. 2e-141;
0; Mismatches 28;
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APPLICANT: MOTILS, David W.
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND ME:
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2002-03-01
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOUTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1355
LENGTH: 1302
TYPE: DNA
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US-10-087-192-1355
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Search completed: June
Job time : 1112 secs
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Best Local S
Matches 477
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Publication No. US20020182586A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 86.6%; Score 477; DB 6; Local Similarity 100.0%; Pred. No. 8e-131; Local 477; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                      697
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US-10-089-641-1 551

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nucleic search, using sw model

GenCore version Copyright (c) 1993 - 2006

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246837 segs, 58886990 residues

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length: length:

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processing: Minimum Match
Maximum Match

100%

Listing first 45

summaries

Pred. No. is the nu score greater than and is derived by a

405. 154. 154. 110.

51

Score

Match

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32740, A

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; TYPE: DNA
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Publication No. US20060099578A1
GENERAL INFORMATION:
APPLICANT: Greenlee, Winner and Sullivan, P.C.
TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
FILE REFERENCE: 98-01 WO
CURRENT APPLICATION NUMBER: US/10/488,619
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 3040
SOFTWARE: Patentin version 3.1
SEQ ID NO 1846
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                                                  ACCTGCACTGCATCCTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTGG
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US-10-953-349-25357
US-10-953-349-34694
US-11-293-397-775
US-10-953-349-35480
US-10-953-349-35480
US-10-953-349-35471
US-10-953-349-34571
US-10-953-349-32119
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US-10-953-349-32119
US-10-953-349-3223
US-10-953-349-28202
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Pred. No. 2.3e-85;
0; Mismatches 62;
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2498, A
2720, A
27211, A
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34694, A
2775, App
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FTWARE: PatentIn Ver. 2.1
ID NO 1
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RRENT FILING DATE: 2005-12-07
IOR APPLICATION NUMBER: US/10/600,158
IOR FILING DATE: 2003-06-20
IOR APPLICATION NUMBER: US/09/534,811
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PELICANT: The Government of the United States of America
PELICANT: As represented by the Secretary of the
PELICANT: Department of Health and Human Services
PELICANT: Department of Health and Human Services
TLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
TLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
TLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
LE REFERENCE: 015280-367100US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AME/KEY: CDS
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THER INFORMATION: protein (GADD45)
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                                      GCGCGTGGGCGATGTGCAGCGGCTGGCGGCTATCGTG-----
                                                                                                     GCTGCAGATCCATTTTACGCTGATCCAGGCTTTTCTGCTGCGAGAACGACATCGACATAGT
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GCGCGTCAGCAACCCGGGCCGGCTGGCGGAGCTCCTGCTCTTGGAGACCGACGCTGGCCC
                                                                                                                                                               CCCCGATAACGTGGTGTTGTGCCTGCTGGCGGCGGACGACGACGACGACAGAGATGTGGC
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Pred. No. 1.6e-27;
0; Mismatches 156;
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APPLICANT: Ludwig Institute for Cancer Research et TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 29967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
INUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
SEQ ID NO 798
LENGTH: 1355
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                         ACATTCATCTCAATGGAAGGATCCTGCCTTAAGTCAACTTATTTGTTTTTTGCCGGGAAAG
                                                                                                                                                                                     - GCCGCCGGCGAGGAGGCGGGTGCCCCGGGCGACCTGCATTCCTCATTTCGAACCC
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TCGCTACATGGATCAATGGGTTCCAGTGATTAATCTCCCTGA
                                                                                                                                                     CGCGGCGAGCGAGCGCCGAGCAGCCCCGGACCTGCACTGCGTGCTGACGAATCC
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Pred. No. 1.6e-27;
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RESULT 4 US-10-488-619-1845/c

Sequence 1845, Application US/10488619

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blication No. US20060099578A1

IPPLICANT: Greenlee, Winner and Sullivan, P.C.

PPLICANT: Greenlee, Winner and Sullivan, P.C.

ITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations

ITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays

ILE REFERENCE: 98-01 WO

URRENT APPLICATION NUMBER: US/10/488,619

URRENT FILING DATE: 2004-03-01

UMBER OF SEQ ID NOS: 3040

DFTWARE: PatentIn version 3.1

ID NO 1845
                                                                                                                                                                                                                                                                         st Local
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"TLE OF INVENTION: SEQUENCE-DETERMINED DNA
"TLE OF INVENTION: ENCONDED THERBY
"LE REFERENCE: 2750-1579PUS2
"RRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE: 2004-09-30
UMBER OF SEQ ID NOS: 40252
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LOCATION: (1)..(609)
CTHER INFORMATION: N IS G,
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                             OPTWARE: PatentIn version 3.3 Q ID NO 36159 LENGTH: 979
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376 CTCATTTCGAACCCCAACGAGGACGCCTGGAAGGATCCCGCCTTGGAGAAGCTCAGCCTG
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165; Conserv
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                                                                                                                                                                                                                                GTGCTGGCTGCGGTGAGGAGGACGAGGGCGACATCGCGCTGCAGATCCATTTTACGCTG
                                                                            ATGATGGCCGAGGCGGACGGGACGGCGACGGCTTCATCAGCCTGCCCGAGTTCGCGGCC 387
                                       CTCAACGCCACGGTGGCCGGCGACGCGGCCGCCGTCGAGGAGGACCTGCGCCACGCCTTC
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Pred. No. 1.4
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Pred. No. 0.00086;
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RESULT 7 US-11-255-290-11

GENERAL INFORMATION:

Thomas

APPLICANT: Evans, APPLICANT: Slatk APPLICANT: Chen,

Slatko, Barton Chen, Lixin Vaisvila, Romaldus Guan, Chudi

APPLICANT:

TITLE OF INVENTION: Repair of Nucleic Acids FILE REFERENCE: NEB-256-US CURRENT APPLICATION NUMBER: US/11/255,290

for Improved

Amplification

Sequence 11, Application US/11255290 Publication No. US20060088868A1

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US-10-953-349-32740
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32740, Application US/10953349 Publication No. US20060107345A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 44.8%;
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 32740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTMARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        568 CAGAACGGCGACGGCCTCATCTCCTTCGACGAGTTCAAGGTCATGATGGCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496 САВСССВВСВВВАССТТВЕТСТВАТСВАСВТВАСВССССВВВВВССТАВАВ
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CACGGCCACCTGCGGCGCGCAACCTGGACCTCATCCGGAGCCTGGGGGCCGACGA
                                     CAGCGTTAACGACTGGGTGCCCAGCATCACCCTCCCCGAGTGACAGCCCGGCGGGGA 509
                                                                                                                                                    GECCEGEGTCEGCCTCEACECCGCCGACEGCCGTCCCAAGAACGTGCTGGTEACCGCEGC 594
                                                                                                                                                                                   CGCGGTGGAGGGCCTGCCTGCCGATCGCCGCGTTCACGGCGCTCGCCGCGCTCAGGGC 534
                                                                                                                                                                                                                                                       CGAGAACGACATCGACATAGTGCGCGTGGGCGATGTGCAGCGGCTGGCGGCTATCGTGGG 332
                                                                                                                                                                                                                                                                                                                                       GGAGGACGAGGGCGACATCGCGCTGCAGATCCATTTTACGCTGATCCAGGCTTTCTGCTG 272
                                                                                                                                                                                                                                                                                                                                                                            AGTCAGCGGCTTCAGCCAGGGCGACAAGGTCATCGCCGTCAACTTCCCGGGGTGGCGGCGG 414
                                                                           CTCGGGCGCGTCGGCACCTTCGCCGTGCAGCTGGCGAGCCTCGCGGGGCACCACCACGT
                                                                                                               CGAGGACGCCTGGAAGGATCCCGCCTTGGAGAGAGCTCAGCCTGTTTTGCGAGGAGAGCCG 452
                                                                                                                                                                                                                                                                                                      GCTGGCCGAGTACGCGGTGGTGCCGGCGTCGCAAGCAGCGCTGAGGCCTCCAGAGGTGTC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41.8; DB 6;
Pred. No. 0.12;
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IRRENT FILING DATE: 2005-10-20
FIOR APPLICATION NUMBER: 60/620,896
FIOR FILING DATE: 2004-10-21
FIOR APPLICATION NUMBER: 60/646,728
FIOR FILING DATE: 2005-01-24
FIOR APPLICATION NUMBER: 60/673,925
FIOR FILING DATE: 2005-04-22
FIOR FILING DATE: 2005
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TLE OF INVENTION: SEQUENCE-DETERMINED DI
TLE OF INVENTION: ENCONDED THERBY
LE REFERENCE: 2750-1579PUS2
RRENT APPLICATION NUMBER: US/10/953,349
RRENT FILING DATE: 2004-09-30
"MBER OF SEQ ID NOS: 40252
                                  NAME/KEY: misc feature OCATION: (217)...(217) CTHER INFORMATION: n is 1-953-349-30766
                                                                                                                                                                                                             OCATION: (214)...(214)
THER INFORMATION: n is
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||uence 30766, Application US/10953349
|lication No. US20060107345A1
|ERAL INFORMATION:
                                                                                                                                                                                                                                                   OCATION: (214)..(214)
                                                                                                                                                                                                                                                                                                                           RGANISM: Triticum aestivum
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US-10-953-349-35342
; Sequence 35342, Application US/10953349
; Publication No. US20060107345A1
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RESULT 10

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FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35182
LENGTH: 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-953-349-35182

Sequence 35182, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED |

TITLE OF INVENTION: ENCONDED THERBY
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; ORGANISM: Zea mays subsp. mays
US-10-953-349-35182
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Best Local Similarity
Matches 116; Conserv
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TCGAG
                              TGGCG 321
                                                             TGGCCATGTTCGGCTCCGAAATCGCCATCGCCTTCAGCGGCGCGGAGGACGTGGCGCTGA
                                                                                       TCCAGGCTTTCTGCTGCGAGAACGACATCGACATAGTGCGCGTGGGCGATGTGCAGCGGC
                                                                                                                             ACGAGGCCCTGGCGCGTGAGCTGGAGGGCGCGCTCGCCGGTGGAGATCATGGATCGGGCGC
                                                                                                                                                            TGCTGGCTGCGGGTGAGGAGGACGAGGGCGACATCGCGCTGCAGATCCATTTTACGCTGA
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Pred. No. 0.29;
0; Mismatches 128;
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HERAL INFORMATION:
PPLICANT: ALEXANDROV, Nickolai et al.
PPLICANT: ALEXANDROV, Nickolai et al.
TILE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TILE OF INVENTION: ENCONDED THERBY
LE REFERENCE: 2750-1579PUS2
URRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE: 2004-09-30
UMBER OF SEQ ID NOS: 40252
DFTMARE: Patentin version 3.3
3 ID NO 35342
                                                                                                                                                                                                                                                                                                                               OFTWARE: PatentIn version 3.1
Q ID NO 29
                                                                                                                                                                                                                                                                                                                                                                    RIOR FILING DATE: 2003-02-04
IMBER OF SEQ ID NOS: 88
                                                                                                                                                                                                                                                                                                                                                                                                    URRENT APPLICATION NUMBER: US/10/525,647
URRENT FILING DATE: 2005-02-24
RIOR APPLICATION NUMBER: EP 03075331.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT: CropDesign N.V. TILE OF INVENTION: Rice promoters TLE REFERENCE: CD-071-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quence 29, Application blication No. US200601: WERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ches 115;
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NOCATION: (468)..(469)
OTHER INFORMATION: n is a,
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                                                                                                                                0-525-647-29
                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: TC89891
                                                                                                                                                                                                                                                          PEATURE:
                                                                                                                                             OCATION: (5). (5)
                                                                                                                                                                NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                               YPE: DNA
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                                                                        Similarity
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                                                       Score 39.4; DI
Pred. No. 0.42,
0; Mismatches
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Sequence 2881, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DN/
TITLE OF INVENTION: SEQUENCE-DETERMINED DN/
TITLE OF INVENTION: SEQUENCE DETERMINED DN/
TITLE OF INVENTION: SEQUENCE US/10/953,349

TURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTMARE: Patentin version 3.3

SEQ ID NO 28881
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US-10-953-349-28360/c
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Publication No. US20060107345A1
GENERAL INFORMATION:
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TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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SOFTWARE: PatentIn version 3.3
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89; Conservative
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                                                                             US/10/953,349
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ENGTH: 1188
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TILE OF INVENTION: ENCONDED THERBY
LE REFERENCE: 2750-15799US2
IRRENT APPLICATION NUMBER: US/10/953,349
IRRENT FILING DATE: 2004-09-30
IMBER OF SEQ ID NOS: 40252
FYWARE: Patentin version 3.3
ID NO 34511
juence 31614, Application US/10953349
ilication No. US20060107345A1
iERAL INFORMATION:
PLICANT: ALEXANDROV, Nickolai et al.
TLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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t Local Similarity
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; TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15795US2
CURRENT APPLICATION UNMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 31614
LENGTH: 1122
TYPE: DNA
ORGANISM: Triticum aestivum
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                                                                                                                                            295 CGCGTGGGCGATGTGCAGCGGCTGGCGGCTATCGTGGGCGCGGCGAGGAGGCGGGTGCG
                                                                              CCGGGCGACCTGCACTGCATCCTCATTTCGAACCCCAACGAGGACGC 401
                                                                                                                CGTGGCGGCGGTGGAAGGGGAAGGGCCGCCATGAAGGGCGCAGCAAGGTGGTCGTGGTG
                                                CCGCACAAGCACGACGCGTCTTCATCGCCAAGGCCAAGGAGGACGC
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4, 2006,
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Search completed: June Job time : 25 secs

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

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826
1 MTLEEVRGQDTVPESTARMQ.....LFCEESRSVNDWVPSITLPE 159
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

9 i;	Score	Query	Length	BB	1	Description
٠ :	826	100.0	159	2	AAW08138	Human
N	826	٠	159	w	AAY87957	Human
w	826	•	159	σ	ABR40340	Abr40340 Human Gad
4	826	•	159	7	ADG62828	Adg62828 Human gro
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7	826	100.0	159	9	ADX85166	Adx85166 Human gad
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9	811	98.2	160	w	AAB13772	Human
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Ξ.	787	95.3	159	σ	ABR40341	
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. 4	737	89.2	141	7	ABM85647	
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9:	710	86.0	158	7	ABM85646	Abm85646 Mouse pro
.7	550	66.6	104	w	AAB34425	
œ	550	66.6	104	w	AAB34424	Aab34424 Gene 41 h
و:	457.5	55.4	165	N	AAR53669	
ŏ	457.5	55.4	165	σ	ABU07405	Abu07405 Protein d
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Human	Novel	Adx85164 Mouse gad	Mouse	Mouse	Respi			Ady20500 PRO polyp			Human									

ALIGNMENTS

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RESULT 1
AAW08138
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
                                                                                                                                                                                                                                              Human cytokine response protein CR6.
                                                                                                                                                                                                                           Cytokine response protein; CR6; interleukin-2; IL-2; ligand-stimulated gene expression; diagnosis; therapy.
                                                                                                                                                                                                                                                            11-MAR-1997
                                                                                                                                                                                                                                                                                       AAW08138 standard; protein;
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                                                                                                            (DART-) DARTMOUTH COLLEGE.
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                                                                                                                          95US-00461379.
95US-00462337.
95US-00462390.
95US-00463074.
95US-00463081.
95US-00465585.
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Cytokine response proteins and genes - used in the detection and therapy of diseases caused by a mutation in the CR coding region.

N-PSDB;

AAT43381.

WPI; 1997-043062/04.

Smith KA,

Beadling

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Claim 6; Page 29-30; 81pp; English.

Cytokine response proteins CR1-CR8 (AAW08133-40) are encoded by genes (see also AAT43376-83) isolated from a thiol-selected interleukin-2-induced human T-cell blast cDNA library. 6 Genes (CR1, 2, 3, 5, 6, 8) are novel. CR6 belongs to a family of small nuclear-localising gene products. It binds to p21 and may facilitate cellular proliferation by preventing the inhibitory activity of p21. Recombinant CR6 polypeptides can be

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20-NOV-1991;
10-AUG-1993;
27-OCT-1994;
05-JUN-1996;
This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine response gene 2 (CR2) and modulates CR2 activity. The products of the invention have cytostatic, anti-allergic, immunosuppressive and antimicrobial activity. The antibodies are useful as therapeutic agents for regulating cellular proliferation and differentiation and for treating all kinds of cancers, immune diseases such as allergic, autoimmune, and rheumatologic diseases, transplant rejection, and as anti-infectives for fighting viral, bacterial, parasitic and fungal infections. This sequence represents the human CR6 protein described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic; immunosuppressive; antimicrobial; therapy; cell proliferation; treatment; cell differentiation; cancer; immune disease; rheumatologic disease; transplant rejection; anti-infective; CR6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91US-00796066.
93US-00104736.
94US-00330108.
96WO-US008992.
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The invention relates to a novel method for modulating pathways leading to programmed cell death, comprising selecting a target within the c-Jun-CC where the comprising selecting with the traget using the terminal kinase (JNK) pathway, and interfering with the traget using the agent that either up regulates or down regulates the JNK pathway. The method of the invention has cytostatic activity. A method of the convention is useful for modulating pathways leading to programmed cell death induced by TNFalpha, Fas, TRAIL, genotoxic agent such as the convention or cisplatinum. Another method of the invention is useful for screening and identifying an agent, preferably peptides, peptide mimetics, peptide-like molecules, mutant proteins, cDNAs, antisense coligonucleotides or constructs, lipids, carbohydrates or synthetic or natural chemical compounds, that modulate JNK pathway in vitro. A method of the invention may also be useful for treating cancer, and for preventing apoptosis. Compounds that are capable of interfering with the ability of Gadd45beta to associate with JNKK2 are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 159;
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Best Local
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N-PSDB; ACC59049.
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12-OCT-2001; 2001US-0328811P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 122-123; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Franzoso G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-2002; 2002WO-US031548
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Pred. No. 3.7e-89;
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The present invention relates to a novel method for assaying modulators of growth arrest and DNA damage-inducible (GADD) 45 proteins. The method involves incubating the compound with GADD45 in agueous solution and determining any inhibition or decrease in the binding of GADD45 gpecifically to a Cdc2 (cell division cycle-2) polypeptide. Inhibition of GADD45, a protein involved in DNA repair, results in increased sensitivity of cancer cells to DNA-damaging agents GADD45 activates a g2/M checkpoint after damage induced by UV radiation or alkylating agents and overexpression of GADD45 in normal fibroblasts arrests cells in G2/M. Compounds that inhibit GADD45 are able to sensitise proliferating cells to DNA-damaging agents, so are useful as adjuncts in treatment of cancer with UV light or chemotherapeutic agents such as cis-platin. Inhibition of GADD45 will allow a reduction in the dose of toxic DNA-damaging agents required to induce apoptosis in cancer cells. The present sequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Growth arrest and DNA damage-inducible gene 45; GADD45; Cdc2; cell division cycle-2; DNA repair; cancer; DNA-damaging agent; therapy; chemotherapeutic agent; cis-platin; apoptosis; cytostatic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In vitro identification of GADD45 modulators, useful for increasing sensitivity of cancer cells to DNA damage, e.g. from effects of compounds
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The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature of the mRNA, and using that gene expression is the patient, where gene expression of at least 60% of the genes correlates with that of the gene expression of at least 60% of further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis; diagnosis or array or gene chip, specific for rheumatoid arthritis; diagnosis or
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                                                                                                                                                                                                                                               Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and trepresentation arthritis, lupus, fibrositis, osteoarthritis, fibromya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                               Thorton SL;
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Pred. No. 3.7e-89;
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                                                                                                                                                                                                                                                  osteoarthritis, fibromyalgia
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analyses of autoimmune disease or rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collagen-induced arthritis; and reducing the symptoms associated with collagen-induced arthritis. The compositions of the invention have the following activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic, antigout, antiinflammatory, dermatological, and immunosmodulatory. The methods and compositions of the present invention are useful for disgousing and treating autoimmune disease or arthritides, such as rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, and an immune disease caused by an infectious agent. This sequence represents a protein sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from
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ry Match
                                                                                                                                                                                                                                                                            Sequence 159
                                                                                                                                                                                                                         Local
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              LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
                                                               VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI 120
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LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                     Score 826; DB 7; Length 159; Pred. No. 3.7e-89;
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ADJ75308 standard; protein; 159 AA.

20-MAY-2004 (first entry)

Marker gene related amino acid sequence SEQ ID NO:560.

bronchial asthma; chronic obstructive pulmonary disease; respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic; therapy; marker.

Homo sapiens.

EP1394274-A2.

03-MAR-2004

04-AUG-2003; 2003EP-00254857

06-AUG-2002; 2002JP-00229312. 20-MAR-2003; 2003JP-00077212.

(GENO-) GENOX RES INC.

Ohtani N, Sugita Y, Yamaya M,

Kubo H,

Nagai H,

Izuhara

WPI; 2004-193155/19

Testing for bronchial asthma or chronic obstructive pulmonary disease comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from healthy subject λ̈́q

Example 11; SEQ ID NO 560; 241pp; English

> Create present invention describes a method of testing for bronchial asthma creation cobstructive pulmonary disease. The method comprises crown in a subject, comparing the expression level of a marker gene in a biological sample creation a subject, comparing the expression level determined with the capression level of the marker gene in a biological sample from a healthy crown a beautiful described; and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial crown and interpretation of the stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (I) for tresting for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (3) a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polymucleotide that suppresses the capression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for corresponding to a portion of caprosic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (I) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention. 밁 Matches Query Match Sequence 159 Local Similarity 121 LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159 159; 61 61 Н VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI MTLEEVRGQDIVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLAVDPDNVTFC VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI MTLEEVRGQDTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE Conservative A, 100.0%; Score 826; DB 8; 100.0%; Pred. No. 3.7e-89; 0; Mismatches 159 Length 159; Indels 0 Gaps 120 60 60

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RESULT 7
ADX85166
ID ADX8

ADX85166 standard; protein; 159 AA.

05-MAY-2005 (first entry)

Human gadd45 protein, seqid:10

Cell death; apoptosis; degeneration; cancer; cytostatic; neoplasm; immunotherapy; chemotherapy; gene therapy; gadd45; Jun N terminal kinase modulator.

Homo sapiens

EP1506784-A1

26-JUL-2004; 2004EP-00017667

25-JUL-2003; 2003US-00626905. 02-DEC-2003; 2003US-0526231P.

(UYCH-) UNIV CHICAGO

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Ine invention relates to methods and compositions for modulating pathways leading to programmed cell death or apoptosis. The method involves selecting a target within the c-Jun-N-terminal kinase (JNK) pathway and interfering the target by an agent that either upregulates or downregulates the JNK pathway. The JNK modulator is effective in treating degenerative disease and cancer. The method and compositions of the invention are useful in immunotherapy, cancer chemotherapy and in gene therapy. The present sequence is the human gadd45 protein which is a modulator of JNK pathway.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human placental protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JAN-2006
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WPI; 2005-808574/82.
N-PSDB; AED73447.
                                                                                                                                                                          07-APR-2003; 2003US-0462047P
                                                                                                                                                                                                                         07-APR-2004; 2004US-00821234
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                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           pre-eclampsia; gynecological
                                                                      Labat I,
                                                                                                                        (NUVE-) NUVELO INC
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                                                                      Tang YT,
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                                                                           Stache-Crain B,
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100.0%; Pred. No. 3.7e-89;
tive 0; Mismatches 0;
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                                                                           Boyle B;
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Sequence 165 AA;

from the USPTO web

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The invention relates to a method for identifying a patient with a higher crisk of preeclampsia. The method comprises: (a) assaying a sample from the patient to determine the level of a mRNA or other polynucleotide within the sample from the patient with an antibody seample from the patient with an antibody that specifically contacting a sample from the patient with an antibody that specifically binds to a polypeptide of AED74025-AED74876 to determine the level of polypeptide within the sample, and comparing the level to a standard. Comprising: (a) an antibody specific for any of the polypeptides of CC comprising: (a) an antibody specific for any of the polypeptides of CC comprising: (a) an antibody specific for any of the polypeptides of ED74025-AED74876 or their fragments; or (b) a polynucleotide sequence comprising any of AED73173-AED74024 coupled to a surface; and (c) a standard for any of the polypeptides of AED74025-AED74876 or any of the polypeptides of antibody specific for any of the polypeptides of antibody specific for any of the polypeptides of antibody specific for any of the polypeptides of AED74025-AED74876 or one or more purified polypeptides of AED74025-AED74876, to ameliorate signs or symptoms of preeclampsia; (2) a pharmaceutical composition comprising and composition sequence or symptoms of preeclampsia; and (3) a method of treating preeclampsia. The composition and method are useful for treating preeclampsia. The present sequence obtained from a minon acid sequence concepts and concepts of the printed specification, but was obtained in electronic format directly of the printed specification, but was obtained in electronic format directly concepts the present sequence abtained in electronic format directly concepts the printed specification, but was obtained in electronic format directly concepts the printed specification, but was obtained in electronic format directly concepts the printed specification.
Identifying a patient with a higher risk of preeclampsia comprises nucleic acid hybridization assay or antibody assay to determine level a specific nucleic acid (mRNA) or polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; SEQ ID NO 1127; 358pp; English.
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RESULT 9 AAB13772 밁 맑 Ş 밁 Matches Human; SYG972; cancer diagnosis; cell differentiation; breast cancer; lymphoma; Alzheimer's disease; Parkinson degenerative nervous disease. Human SYG972 protein. 20-JUN-2001 AAB13772 standard; protein; 160 AA. 159; 121 LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159 67 61 VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI 7 ب Similarity MTLEEVRGODTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 165 Conservative (first entry) 100.0%; 0, Score 826; DB 9; Pred. No. 3.9e-89; Mismatches 0 Length 165; Indels cytostatic; n's disease; 0 Gaps 126 120 66 60

Misc-difference

/note= 8

Misc-difference Misc-difference Homo sapiens

Location/Qualifiers

/note=

"Encoded by ACC" "Encoded by GAC"

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The present sequence is the protein sequence for the human SYG972 gene. SYG972 protein is involved in cell differentiation. SYG972 gene is highly expressed in normal differentiated tissues. However, in cancerous tissues, SYG972 gene expression is inhibited. This characteristic of SYG972 gene expression may be used in cancer diagnosis, especially breast cancer. In addition, the SYG972 gene may be used in distinguishing B cells and T cells in determining the origin of cancer in various lymphomas. SYG972 gene and promoter are useful for designing and screening drugs to promote or inhibit apoptosis and differentiation of cells, especially to screen drugs to treat diseases where cell differentiation and apoptosis occur abnormally e.g. cancer, Alzheimer's disease, Parkinson's disease and degenerative nervous diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ry Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-1998;
30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-DEC-1999;
                                                                          GRP17 gene; Gadd45 and MyD118 releated protein; human; cell growth arrest; DNA damage; cancer; apoptosis; aut diagnosis; therapy; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosis of cancer using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-431614/37
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                                                                                                                                                                        17-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page
                                              Homo sapiens
                                                                                                                                                                                                                                     AAW23533 standard; protein; 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                          associated with cell growth arrest and DNA damage
                                                                                                                                                                        (first entry)
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98KR-00063958.
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Location/Qualifiers 40. .69
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98.7%;
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Pred. No. 2.2e-87;
0; Mismatches 2
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                                                                                            apoptosis; autoimmune
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This protein comprises novel human GRP17 (Gadd45 and MyD118 related protein, 17 kDa), a protein encoded by a gene associated with arrest of cell growth and induction of DNA damage. The amino acid sequence was deduced from cDNA clone GEN-554H06 (see AAT74047-48) isolated from a human placental cDNA library. GRP17 protein shows 55% identity with gadd45 and 52% identity with MyD118, both of which are tumour suppressors. It can be expressed in the usual vector/host cell systems. The GRP17 gene is useful for the diagnosis and treatment of cancer, malformations and autoimmune diseases, as well as for screening drugs fo treatment of these conditions. Recombinant GRP17 protein can be used to treate antibodies for the purification, assay and identification of GRP17
                                                                                                   Mouse; c-Jun-N- terminal kinase pathway; JNK pathway; cytostatic; programmed cell death; TNFalpha; Fas; TRAIL; genotoxic agent; cance apoptosis; Gadd45beta; JNKK2; chronic inflammatory disease; Gadd45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New GRP17 gene associated with arrest of cell growth and induction of DNA damage - useful for diagnosis and treatment of cancer, auto-immune diseases etc., also for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 8; 12pp; English
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                                                                                                                                                                                        Mouse Gadd45
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                                                                               autoimmune condition
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                                                                                                                                                                                      SEQ ID NO:
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98.1%;
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Pred. No. 1.5e-86;
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Mus musculus

WO2003028659-A2

02-OCT-2001; 2001US-0326492P. 12-OCT-2001; 2001US-0328811P. 02-OCT-2002; 2002WO-US031548 10-APR-2003

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The invention relates to a novel method for modulating pathways leading to programmed cell death, comprising selecting a target within the c-Jun-N- terminal kinase (JNK) pathway, and interfering with the target using an agent that either up regulates or down regulates the JNK pathway. The method of the invention has cytostatic activity. A method of the invention is useful for modulating pathways leading to programmed cell death induced by TNFalpha, Fas, TRAIL, genotoxic agent such as deunorubicin or cisplatinum. Another method of the invention is useful for screening and identifying an agent, preferably peptides, peptide mimetrics, peptide-like molecules, mutant proteins, cDNMs, antisense oligonucleotides or constructs, lipids, carbohydrates or synthetic or natural chemical compounds, that modulate JNK pathway in vitro. A method of the invention may also be useful for treating cancer, and for preventing apoptosis. Compounds that are capable of interfering with the ability of Gadd4sbeta to associate with JNKK2 are useful for treating human diseases such as chronic inflammatory, and autoinmune conditions and certain types of cancer. The present sequence is used in the
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respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic; gene therapy; marker.
                                                               bronchial asthma; chronic obstructive pulmonary disease;
                                                                                                                        Marker gene related amino acid sequence SEQ ID NO:1387.
                                                                                                                                                                                               20-MAY-2004
                                                                                                                                                                                                                                                                                                                        ADJ76135 standard; protein; 159
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Pred. No. 1.6e-84;
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The present invention describes a method of testing for bronchial asthma CC or chronic obstructive pulmonary disease. The method comprises CC determining the expression level of a marker gene in a biological sample CC from a subject, comparing the expression level determined with the CC expression level of the marker gene in a biological sample from a healthy CC expression level of the marker gene comprises: (a) a group of CC obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial CC genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are composed to the properties of the marker gene when respiratory epithelial cells are composed for bronchial asthma or chronic obstructive pulmonary disease; (c) a kit for screening for a candidate compound for a therapeutic agent composed for bronchial asthma or chronic obstructive pulmonary disease; (d) a animal model for bronchial asthma or chronic obstructive pulmonary disease; (d) a marker gene or an animal model for bronchial asthma or chronic obstructive pulmonary disease; (d) a sthma or chronic obstructive pulmonary disease; (d) a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the compound, a protein encoded by a marker gene; and (7) a DNA chip for testing for composition of the present inventive pulmonary disease, on which a protein encoded by a marker gene; and (7) a DNA chip for testing for composition of the present of the present invention.

CC and antiasthma or a chronic obstructive pulmonary disease, on which a protein encoded by a marker gene; and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for conditions.
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                                                                                                                                                                                                                           Matches 152;
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Best Local :
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20-MAR-2003; 2003JP-00077212
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                                                                                                                                                                                                                                                                                                             Sequence 159 AA;
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                                                                                                                                                                                                                                                 Local Similarity
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LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
                                                    VLAADEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGADEEGGAPGDLHCI
                                                                                          VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI 120
                                                                                                                                                                MTLEEVRGODTVPESTARMOGAGKALHELLLSAQROGCLTAGVYESAKVLNVDPDNVTFC 60
                                                                                                                                          MTLEEVRGQDTVPESTARMQGAGKALHELLLSAHGQGCLTAGVYESAKVLNVDEDNVTFC 60
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                                                                                                                                                                                                                                               Score 787; DB 8;
Pred. No. 1.6e-84;
                                                                                                                                                                                                                              Mismatches
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LISNPHEDTWKDPALEKLSLFCEESRSFNDWVPSITLPE 159

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The invention relates to methods and compositions for modulating pathways leading to programmed cell death or apoptosis. The method involves selecting a target within the c-Jun-N-terminal kinase (JNK) pathway and interfering the target by an agent that either upregulates or downregulates the JNK pathway. The JNK modulator is effective in treating degenerative disease and cancer. The method and compositions of the invention are useful in immunotherapy, cancer chemotherapy and in gene therapy. The present sequence is the mouse gadd45 protein which is a modulator of JNK pathway.
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02-DEC-2003; 2003US-0526231P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wethod for modulating pathways leading to programmed cell death for creating cancer, by obtaining peptide having specific amino acid sequence and regulating JNK pathway using peptide or composition developed using peptide sequence.
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N-PSDB; ADX85167.
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ABM85647;
                                                  ABM85647 standard; protein; 141 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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Pred. No. 1.6e-84;
0; Mismatches 7;
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TXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel DNA and protein sequences which care associated with carcinomas. The sequences are useful for: (i) for CC are associated with carcinomas. The sequences are useful for: (i) for CC screening drug candidates; (ii) for screening of bioactive agent capable of bioactive agent capable of modulating the activity of CAP; (iv) for carcinoma; (vi) for inhibiting the activity of CAP; (iv) for treating CC carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for CC (A genes are useful as DNA vaccines and the CAP are useful as markers of CC carcinoma including lymphoma. The present sequence is one such CAP. Note: CC This patent is an equivalent to basic patent US2002182586A1, for which no CC carcinome and the cAP are useful as markers of CC carcinoma including lymphoma. The present sequence is one such CAP. Note: CC sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 141; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein sequence hCP1767168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; SEQ ID NO 1356; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002; 2002US-00087192
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                           Huntingtons chorea interaction partner #20.
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                                                                10-MAR-2005
                                                                                                                               ADV77059 standard; protein;
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                                                                                                                                                                                                                                                                                                                     79
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genetic disorder; neurological disease; Nootropic; Anticonvulsant;

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Huntingtons chorea; protein structure.
WO2004113566-A2
                                      Homo sapiens.
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29-DEC-2004

18-JUN-2004; 2004WO-EP006617

20-JUN-2003; 2003EP-00013957.

(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN. (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

Wanker E, Lalowski M; Lehrach H, Goehler H, Stroedicke M, Stelzl U;

WPI; 2005-057993/06.

Generating a protein-interaction network of huntingtin, useful for diagnosing and treating Huntington's disease, comprises contacting (poly) peptides with the disease-related (poly) peptides.

Disclosure; Fig 6; 161pp; English.

The invention relates to a method of generating a network of direct and indirect interaction partners of a disease-related (poly)peptide comprises contacting a selection of (poly)peptides suspected to contain direct or indirect interaction partners with the disease-related (poly)peptides and optionally with known direct or indirect interaction partners of the disease-related (poly)peptide. The molecule, (poly)peptide, and antibody are useful for preparing a pharmaceutical composition for the treatment of Huntingtons chorea. The method is useful for generating a network of direct and indirect interaction partners of a disease-related (poly)peptide. The protein, composition, and methods are useful for diagnosing and treating Huntingtons chorea. The present segeunce represents the amino acid sequence of an interaction partner of Huntingtons chorea.

Sequence 185 AA;

*Y Match 88.1%; Score 728; DB 9; Length 185; t Local Similarity 98.6%; Pred. No. 1.9e-77; "ches 140; Conservative 0; Mismatches 2; Indels 0; Gaps

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ALIGNMENTS

DNA-damage-inducible protein gadd45 - Chinese hamster C;Species: Cricetulus griseus (Chinese hamster) C;Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 11-Jan-2000 C;Accession: B39617

B39617

R;Papathanasiou, M.A.; Kerr, N.C.K.; Robbins, J.H.; McBride, O.W.; Alamo Jr., Mol. Cell. Biol. 11, 1009-1016, 1991
A;Title: Induction by ionizing radiation of the gadd45 gene in cultured human A;Reference number: A39617; MUID:91117202; PMID:1990262

cultured human cells:

la

PID

I.; Barre

A; Molecule type: mRNA A; Residues: 1-165 < PAP>

A; Accession: B39617

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A;Cross-references: UNIPARC:UPI000012AF8B; GB:M60973; NID:g191079; PIDN:AAA36984.1; A;Note: the source is Chinese hamster ovary cells C;Superfamily: human DNA-damage-inducible protein gadd45
                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-155 <RES>
A;Cross-references: UNIPROT:P24523; UNIPARC:UPI000012AF8B; GB:L25339; NID:g409032; PIDN
                                                                                                                                                   C;Accession: I48111
R;Hollander, M.C.; Alamo, I.; Jackman, J.; Wang, M.G.; McBride, O.W.; Fornace, J. Biol. Chem. 268, 24385-24393, 1993
A;Title: Analysis of the mammalian gadd45 gene and its response to DNA damage. A;Reference number: I48111; MUID:94043278; PMID:8226988
A;Accession: I48111
                                                                                                                                                                                                                                                                               DNA-damage-inducible protein gadd45 - long-tailed hamster
C;Species: Cricetulus longicaudatus (long-tailed hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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Ron,

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le: Induction by ionizing radiation of the gadd45 gene in cultured human arence number: A33617; MUID:91117202; PMID:1990262
assion: A39617
ies: Mus musculus (house mouse)
19-Oct-1995 #sequence_revision 19-Oct-1995
2: 19-Oct-1995 #sequence_revision 19-Oct-1995
2: 19-Oct-1995 #sequence_revision 19-Oct-1995
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ss-references: GDB:127967; OMIM:126335
position: 1p31.2-1p31.1
rons: 15/2; 49/2; 128/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ries: Homo sapiens (man)
s: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114
                                                                                                                                                                                                                                                                                                                                61 VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIV------GAGEEAG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                91;
                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTLEEVRGQDTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-165 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIV-----GAGEEAGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTLEEFSAAE----QKTERMDTVGDALEEVLSKARSORTITVGVYEAAKLLNVDPDNVVLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTLEEVRGQDTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - PGDLHCILISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE
                                                                                                                                                                                                           QPPDLHCVLVINPHSSQWKDPALSQLICFCRESRYMDQWVPVINLPE 164
                                                                                                                                                                                                                                                     APGDIHCILISNPNEDAWKDPALEKISLFCEESRSVNDWVPSITIPE 159
                                                                                                                                                                                                                                                                                             LLAADEDDDRDVALQIHFTLIQAFCCENDINILRVSNPGRLAELLLLETDAGPAASEGAE
                                                                                                                                                                                                                                                                                                                                                                                 MTLEEFSAGE----QKTERMDKVGDALEEVLSKALSQRTITVGVYEAAKLLNVDPDNVVLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human DNA-damage-inducible protein gadd45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 463.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 457.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                     #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cultured human cells:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:AAA72045.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                              A; Introns:
                                                                                                                                                 A; Gene: GADD45
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Best Local
                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 06
                                          Similarity
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k;Zhan, Q.; Lord, K.A.; Alamo Jr., I.; Hollander, M.C.; Carrier,
Mol. Cell. Biol. 14, 2361-2371, 1994
A;Title: The gadd and MyD genes define a novel set of mammalian
A;Reference number: A56535; MUID:94187707; PMID:8139541
A;Accession: B56535
A;Status: preliminary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P48316; UNIPARC:UPI0000001902; GB:L28177; NID:g456100; R;Alimzhanov, M.B.; Kuprash, D.V.; Turetskaya, R.L.; Osipovich, O.A.; Borodulina, C Dokl. Akad. Nauk 33, 788-791, 1993
A;Title: Cloning and characterisics of murine genes coding for the human GADD45 and R;Reference number: 149679; MUID:94154610; PMID:7509226
                                                                                                                                                                                                                                                                                                                                                                  A;Gene: Gadd45
A;Introns: 15/2; 49/2; 128/3
C;Superfamily: human DNA-dam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-165 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-165 <ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: I49679
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: UNIPARC:UPI0000001902; EMBL:U00937; NID:g392933; PIDN:AAC27351.1;
118 QTPDLHCVLVTNPHSSQWKDPALSQLICFCRESRYMDQWVPVINLPE
                                      114 -PGDLHCILISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE
                                                                                        1 MTLEEVRGODTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                  MTLEEFSAAE---QKTERMDTVGDALEEVLSKARSQRTITVGVYEAAKLLNVDPDNVVLC
                                                                                                                                                                                                                                                                                                                                                                     human DNA-damage-inducible protein gadd45
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                  54.7%;
53.9%;
                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                    Score 451.5; DB 2
Pred. No. 4.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I.; Hollander, M.C.; Carrier, F.;
                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                            165;
       164
                                                  159
                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GADD45 analog
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A;Cross-references: UNIPROT:P48317; UNIPARC:UPI000012AF8D; EMBL:L39010; NID:g1161227; PIA;Note: the authors translated the codon ATC for residue 13 as Met and CGG for residue 2 R;Yoshida, T.; Schneider, E.L.; Mori, N. Gene 151, 253-255, 1994
A;Title: Cloning of the rat Gadd45 cDNA and its mRNA expression in the brain.
A;Reference number: I53907; MUID:95129870; PMID:7828885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Feb-1997 #sequence_revision 13
C;Accession: S68690; I53907
                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-165 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Yoshida, T.; Okazaki, T.; Hughes, P.E.; Schneider, E.L.; FEBS Lett. 380, 87-92, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-165 < YOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Cloning of rat GADD45 gene and induction analysis A; Reference number: S68690; MUID:96181674; PMID:8603754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GADD45 protein - rat
                                                                                                       C; Superfamily: human
                                                                                                                                                                                                               A;Cross-references: UNIPARC:UPI000012AF8D; GB:L32591;
                                                                                                                                                                                                                                                                                                                 A; Accession: I53907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S68690
                                                                                                                                     15/2; 49/2; 128/3
                                                                                                       DNA-damage-inducible protein gadd45
52.8%; Sco
52.4%; Pro
ative 25;
     Score 436.5;
Pred. No. 1.2e
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-Mar-1997 #text_change
     DB 2;
.2e-34;
les 42;
                                                                                                                                                                                                               NID:g799327;
                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          following
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                                                         165;
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                                                                                                                                                                                                                    PIDN: AAA96332.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ionizing radiation
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Indels

13;

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ry Match
t Local s
ches 30
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1e: Sequence and expression of a cDNA encoding MyD118: a novel myeloid differential erence number: A43813; MUID:91125871; PMID:1899477
:ession: A43813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cies: Mus musculus (house mouse)
e: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change (ession: A43813 total, A.; Lord, K.A.; Hoffman-Liebermann, B.; Liebermann,
                                                                                                                                                                                                                                                                                                                      cies: Sus scrofa domestica (domestic pig)
e: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
ession: JC4159; S57497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ry Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss-references: UNIPROT:P22339; UNIPARC:UPI00000213B5; GB:X54149; NID:g53290; PIDN:erfamily: human DNA-damage-inducible protein gadd45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :idues: 1-160 <ABD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tus: preliminary
                                                                                                                                                                                    ecule type: mRNA
idues: 1-132 <ZAC>
                                                                                                                                                                                                                          h, O.R.F.; Bauer, H.C.; Richter, K.; Webersinke, G.; F. 159, 277-278, 1995
Le: Sequence of the porcine full-length cDNA encoding erence number: JC4159; MUID:95347612; PMID:7622064
:ession: JC4159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 protein -
                                                                       verfamily: rat ribosomal protein S12 words: protein biosynthesis; ribosom
                                                                                                                                                 ss-references: UNIPROT:P46405; UNIPARC:UPI000000096F; EMBL:X79417; NID:g872314;
erimental source: endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                 omal protein S12 - pig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 DLHCILISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTLEEVRGQDTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphoprotein
 30; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTP-DLHCVLVTNPHSSQWKDPALSQLICFCRESRYMDQWVPVINLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAPGDLHCILISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTLEEFSAAE---QKIERMDTVGDALEEVLSKARSQRTITVGVYEAAKLLNVDPDNVVLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTLEEVRGQDTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLHCLLVTNCHTDSWKSQGLVEVASYCEESRGNNQWVPYISLEE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTLEELVASD---NAVQKMQAVTAAVEQLLVAAQRQDRLTVGVYEAAKLMNVDPDSVVLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse
12.5%; Score 103.5; ilarity 25.4%; Pred. No. 0.0 Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                      H.C.; Richter, K.; Webersinke, G.; Bauer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 436; DB 2; Length 160 Pred. No. 1.3e-34;
                                                                             ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
   Mismatches
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                       .0097
                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
 46;
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                                     Length 132;
     Indels
                                                                                                                                                                                                                                                                      ribosomal
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     13;
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     Gaps
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63

AAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAG---

--APGDL

117

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A; Map position: 3
A; Introns: 127/3
C; Superfamily: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 150, 331-333, 1994
A;Title: Identification and characterization of a cDNA encoding A;Reference number: I51557; MUID:95121924; PMID:7821801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: I51557
R;Seery, L.T.; Schoenberg, D.R.; Canning, M.B.; Whitehead, Gene 150, 331-333, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribosomal protein S12 - African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-132 <SEE>
                                Ś
                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-145 <HAR>
A;Cross-references: UNIPROT:O14062; UNIPARC:UPI0000
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                                                                                                                                                                                                                                                                                                                                 A;Reference number: Z22007
A;Accession: T41651
                                                                                                                                                                                                                                                                                                                                                                       R;Harris, D.; Wood, V.; Rajandream, submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T41651
                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                40s ribosomal protein s12 - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                          A;Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                          Query Match
Best Local
                                                                                                                                                                                                      Gene: SPDB:SPCC962.04
                                                                                                                                                                                                                         Genetics:
                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 WKDPALEK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
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31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCENDIDIVRYGDYQRLAAIYGAG--EEAGAPGDL---HCILISNPNEDAWKDPALEK 137
                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QAKDVIEE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PMYVKLVEALCAEPQINLIKVDDNKKLGEWVGLCKIDREGKPRKVVGCSCVVVKDYGKES 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STARMQGAGKALHELILSAQRQGCLTAGVYESAKVLNVDPDNVTFCVLAAGEEDEGDIAL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAEHQINLIKVDDNKKLGEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALQEVLKTALIHDGLARGIREAAKAL--DKRQAHLCVLASNCDE-----PMYVKLVEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAG--EEAGAPGDL---HCILISNPNEDA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAGGVMDVNTALQEVLKTALIHDGLARGIREAAKAL--DKRQAHLCVLASNCDE-----
                                    LEEVRGODTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFCVL
                                                                                                                                                  rat ribosomal protein S12
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                        UNIPROT:014062; UNIPARC:UPI0000132ECE; EMBL:AL031323; PIDN:CAA20436
:e: strain 972h-; cosmid c962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.3%;
                                                                           12.2%; Score 101; DB 2;
26.5%; Pred. No. 0.019;
tive 25; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101.5; DB
Pred. No. 0.015;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         August
                                                                                                                                                                                                                                                                                                                                                                                            M.A.; Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                              51;
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                                                                                                             Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 132;
                                                                              Indels
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                                                                         32;
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                                                                              Gaps
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recombinase, ATPase [imported] - Clostridium acetobutylicum ries: Clostridium acetobutylicum ries: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 riesion: A97124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cies: Arabidopsis thaliana (mouse-ear cress)
s: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
sssion: D84577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee ly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. zteriol. 183, 4833-4838, 2001
Le: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clerence number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                   le: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. erence number: A84420; MUID:20083487; PMID:10617197 ession: D84577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ole recA protein [imported] - Arabidopsis thaliana
cies: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 idues: 1-349 <KUR>
ss-references: UNIPROT:P58254; UNIPARC:UPI00001334DE; GB:AE001437; PIDN:AAK79780.1
erimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                          e: At2g19490
position: 2
                                                                                                                                                                                                                                                                                                                                                                                   X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Do, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C. 2402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ry Match
                                                                                                                                     erfamily: recombination protein recA
                                                                                                                                                                                                                               ss-references:
                                                                                                                                                                                                                                                                     scule type: DNA
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                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 PESSGK---TTVÄLH-ILAEÄQKKGGAAÄFIDAEHALDPQYÄRALGVDIDN-----LVVS 116
  20
                                          l Similarity
42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEDAWKDPALEKLSLFCEESRSV 148
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QGAGK---ALHELLLSAQRQG--CLTAGVYES----AKVLNVDPDNVTFCVLAAGEEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPDTGEQALEIAEALVRS----GAIDVIVVDSV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -QARLMSQALRKLTGSINKSKCI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombination protein recA
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                                             Conservative
                                                                                                                                                                                                                                                     <STO:
                                                                                                                                                                                                                             UNIPROT:Q9ZUP2; UNIPARC:UPI00000A2BE8; GB:AE002093; NID:g4191779; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.4%; 29.4%;
                                                           11.4%;
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                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 94; DB 2;
Pred. No. 0.23;
2; Mismatches 5
                                                             Score 94; DB 2
Pred. No. 0.25;
                                             Mismatches
                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                          45;
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                                                                                        Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 349
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                                             Indels
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                                          38;
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                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
  69
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C;Species: Nus musculus (house mouse)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_ch
C;Accession: S05492
R;Ayane, M, Nielsen, P.; Koehler, G.
Nucleic Acids Res. 17, 6722, 1989
A;Title: Cloning and sequencing of mouse ribosomal protein
A;Reference number: S05492; MUID:89385996; PMID:2780296
A;Molecule type: mRNA
A;Residues: 1-132 <AVA>
A;Residues: 1-132 <AVA
A;Residues: 1
A;Cross-references: UNIPARC:UPI0000173A2B
A;Note: the protein is designated as ribosomal
C;Superfamily: rat ribosomal protein S12
C;Keywords: blocked amino end; protein biosynth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_c;Accession: S13074; A27426; A33221
R;Wool, I.G.; Chan, Y.L.; Paz, V.; Olvera, J.
Biochim. Biophys. Acta 1050, 69-73, 1990
A;Title: The primary structure of rat ribosomal proteins: A;Reference number: S13071; MUID:91002678; PMID:2207170
A;Accession: S13074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P09388; UNIPARC:UPI0000163873; C;Superfamily: rat ribosomal protein S12 C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A27426;
A;Accession: A27426
A;Molecule type: mRNA
A;Residues: 1-130 <LIN>
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R3MS12
ribosomal protein S12 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P09388; UNIPARC:UPI0000163873; EMBL:M18547 R;Lin, A.; Chan, Y.L.; Jones, R.; Wool, I.G. J. Biol. Chem. 262, 14343-14351, 1987 A;Title: The primary structure of rat ribosomal protein S12. The relational control of the primary structure of the primary structure of the relations of the primary structure of the primary structure of the relations of the primary structure of the primary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-132 < WOO>
                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 2-130 <LIN2>
                                                                                                                                                                                                                                                                                                                                                                                              A; Note: this sequence has A; Accession: A33221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UPI00001679A3; EMBL:M18547; NID:g206740; PIDN:AAA42077.1;
A;Note: this sequence has been revised in reference S13071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ribosomal protein S12, cytosolic [validated] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 ALQEVIKTALIHDGLARGIREAAKAL--DKRQAHLCVLASNCDE-----PMYVKLVEAL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 ALHELLISAQRQGCLTAGVYESAKVLNVDPDNVTFCVLAAGEEDEGDIALQIHFTLIQAF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EASGKTTLALH-VIAEAOKOGGTCVFVDAEHALDSSLAKAIGVNTEN-----LLLSQPDC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEQALSLVDTLIRS----GSVDVIVVDSV---AALVPKGELEGEMGDAHMAM-----QAR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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             protein biosynthesis; ribosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the amino acid sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The relationship of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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S12

52

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PIDN

30/Product: ribcsomal protein S12 #status experimental <MAT> codified site: blocked amino end (Ala) (in mature form) #status experimental

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cription: plays an essential role in homologous recombination, in induction of the erfamily: recombination protein recA words: ATP; DNA binding; DNA recombination; DNA repair; nucleotide binding; P-loop 76/Region: nucleotide-binding motif A (P-loop) 1148/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ernate names: recombinase A cies: Acetobacter polyoxogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ession: JN0639
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                                                                                               cription: The sequence of erence number: Z21502 ession: T34303
                                                                                                                                                                                                                                                          hetical protein F54E7.2 - Caenorhabditis elegans cies: Caenorhabditis elegans e: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               etics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss-references: UNIPROT: Q08327; UNIPARC: UPI00001334C0; GB: D13183; NID: g391591; PIDN
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le: Cloning and sequencing the recA+ genes of Acetobacter polyoxogenes and Acetoba erence number: JN0639; MUID:93252279; PMID:8486287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ama, K.; Fukaya, M.; Takemura, H.; Okumura, H.; Kawamura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                          :ession: T34303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ry Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ession: JN0639
                                          ecule type: DNA
                                                                                                                                                        tted to the EMBL Data Library, June 1994 cription: The sequence of C. elegans cosmid
ss-references: UNIPARC:UPI0000177296; EMBL:U00067; PIDN:AAC77514.1; GSPDB:GN00021;
                         dues: 1-145 <BEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 EEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGD----LHCIL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAEHQINLIKVDDNKKLGEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCENDIDIVRVGDVQRLAAIVGAG--EEAGAPGDL----HCILISNPNEDAWKDPALEK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPDAGEQALEIADTLVRS----GAVDVLVVDSV---AALVPRAELEGDMGDSHVGLHARL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALHELLLSAQRQCCLTAGVYESAKVLNVDPDNVTFCVLAAGEEDEGDIALQIHFTLIQAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSQ-----ALRKLT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISNPNEDAWKDPALEKLS 139
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                                                                            GB/EMBL/DDBC
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A; Map position: 3
A; Introns: 57/2
C; Superfamily: rat ribosomal
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A,Gene: CESP:F54E7.2
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Search completed: June Job time: 23 secs
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                                                                                      61 VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVG
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Q2HZD5 CHICK
Q8UUP4 XENLA
Q6DLJ3 XENTR
Q7ZXC4 XENLA
Q6DLJ3 XENTR
Q7ZXC4 XENLA
Q6PQ21 BRARE
Q4RYO TETNG
Q6MM1 BRARE
Q1GM1 BRARE
Q1GM6 CHICK
Q7ZX24 XENLA
Q4T9H6 TETNG
Q2HZD6 CHICK
Q7ZX24 KENLA
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Q2HZD6 CHICK
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AND VARIANT SER-1	enBank/DDBJ databas	in BD Creator(TM)	ra D., Kelley T., LaBae	י (טט).		Zhao Y., Yang J., Xu chromosome 9q22.1q2	SER-112.	EMBL/GenBank/DDBJ database	Hong S., Lee H., Bae Gadd45 gamma gene and		regulates	1; DOI=10.1038/sj.onc.	ily of stress-inducible GADD45-like proteins medi stress-responsive MTK1/MEKK4 MAPKKK."; 5:521-530(1998).	16/8009	\coop_0		lata; Vertebrata; Euteleostomi; ss; Primates; Catarrhini; Hominida		protein GADD45	otKB/Swiss-Prot.	159 AA.	ALIGNMENTS							
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TIN, 604949; gene.

YIM, 604949; gene.

30; GO:0005515; F:protein binding; IPI.

30; GO:0000585; P:activation of MARKKK activity; TAS.

30; GO:0000581; P:DNA repair; TAS.

30; GO:0006581; P:DNA repair; TAS.

InterPro; IPR004038; Ribosomal LTA.

Pfam; PF01248; Ribosomal LTA.

Pfam; PF01248; Ribosomal LTA.

Pfam; PF01248; Ribosomal LTA.

Pfam; PF01248; Ribosomal LTA.

Orowth arrest and DNA-damage-inducible protein GADD45 gamma.

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                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
ry Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.; "NIEBS-SNPs, environmental genome project, NIEBS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu)."; Jubmitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                        SEQUENCE
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AAM030007.1; -; I
AAM03058.1; -; I
AAM19325.1; -; I
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QR -> HG (in Ref. 4).

APG -> CAC (in Ref. 4).

26427E5881941E64 CRC64;
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RESULT
OF VERSON

ID VERSON

ID VERSON

ID TO THE PROPERTY OF 
RESULT 3
Q6IAW6 HUMAN
ID Q6IAW6;
AC Q6IAW6;
DT 05-JUL-2
DT 07-FEB-2
DT 07-FEB-2
DE GADD45G
GN Name=CAD
OS HOmo sap
OC Eukaryot
OC Mammalia
OC Homo.
OX NCBI_Tax
RN [1]
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Best Local S
Matches 159
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87 HUMAN
Q5VZ87 HUMAN
                                                                                                                                                                                                                                                                       Q6IAW6 HUMAN
Q6IAW6;
05-JUL-2004,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2005, integrated into UniProtKB/T 10-MAY-2005, sequence version 1. 07-FEB-2006, entry version 4. Growth arrest and DNA-damage-inducible, Name=GADD45G; ORFNames=RP11-26016.1-001;
                                                                             Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                             GADD45G protein.
Name=GADD45G;
                                                                                                                                                                                                                   05-JUL-2004, sequence version 07-FEB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004038; Ribosomal_L7A.
Pfam; PF01248; Ribosomal_L7Ae; 1.
SEQUENCE 159 AA; 17121 MW; 2642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL161910; CAH71791.1; -; Genomic_DNA. Ensembl; ENSG00000130222; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
  NCBI_TaxID=9606, [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q5VZ87
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                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Homin
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Pred. No. 3e-71;
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01-MAY-2000, sequence version
07-FEB-2006, entry version 16.
Gadd45-related protein.
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InterPro; IPR004038; Ribosomal L7A.
Pfam; PF01248; Ribosomal L7Ae; 1.
SEQUENCE 159 AA; 17107 MW; 27F27E58
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Ebert L., Schick M., Neubert P., Schatten R., Henze S., Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                   EMBL; D83023; BAA84543.1; -; mRNA.
Ensembl; ENSG00000130222; Homo sapiens
InterPro; IPR004038; Ribosomal_L7A.
                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/teDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                      GRP17, highly homologous to huma J. Hum. Genet. 44:300-303(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99426078; PubMed=10496071; DOI=10.1007/s100380050164; Suzuki M., Watanabe T., Fujiwara T., Nakamura Y., Takahashi E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=GRP17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning, expression, and mapping of a novel human cDNA, GRP17, highly homologous to human gadd45 and murine MyD118.";
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                                                                                                                                                                                                                                            PF01248;
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VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI
                                                                                              MTLEEVRGODTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC
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                                                                       MTLEEVRGQDTVPESTARMQGAGKALHELLLSAHGQGCLTAGVYESAKVLNVDPDNVTFC
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                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                            Ribosomal_L7Ae;
AA; 17031 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Buteleostomi;
Buarchontoglires; Primates; Catarrhini; Hominidae;
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98.7%;
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Pred. No. 5.9e-71;
                                                                                                                                                       Score 814; DB 2; 1
Pred. No. 4.3e-70;
0; Mismatches 2;
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27F27E5881941E64 CRC64;
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Q9ROSO MUUSE
ID Q9ROSO MAC Q9ROSO MAC Q9ROSO DT 01-MAY-2
DT 01-MAY-2
DT 07-FEB-2
DT 07-FEB
RESULT 6
GA45G_RAT
ID GA45G_RAT
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REMBL; AY258502; AAP79506.1; -; Genomic DNA.

REMBL; BNSMUSG00000021453; Mus musculus.

REMBC1346325; Gad4459.

REMGI; MG1:1346325; Gad4459.

REMG1:0005634; C:nucleus; TAS.

REMG1:00005636; P:protein binding; IPI.

REMG1:00001666; P:protein binding; IPI.

REMG1:00001666; P:interferon-gamma biosynthesis; TAS.

REMG1:0000074; P:regulation of protein kinase activity; IDA.

REMG1:0000074; P:regulation of protein kinase activity; IDA.

REMG1:0000074; P:regulation of progression through cell cycle; IDA.

REMG1:0000074; P:repulation of progression through cell cycle; IDA.

REMG1:000074; P:repulation of progression through cell cycle; IDA.

REMG1:000075; IPR004038; Ribosomal I/A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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07-FEB-2006, entr
OIG37 (GADD45G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129/Sv;
Balliet A.G., Hollander M.C., Fornace A.J. Jr.,
Liebermann D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99386956; PubMed=10455148; DOI=10.1074/jbc.274.35.24766; Nakayama K., Hara T., Hibi M., Hirano T., Miyajima A.; "A novel oncostatin M-inducible gene OIG37 forms a gene family w. MyD118 and GADD45 and negatively regulates cell growth."; J. Biol. Chem. 274:24766-24772(1999).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
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Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9ROSO MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                          LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
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96.9%;
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Pred. No. 1.2e-68;
0; Mismatches 5
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STANDARD;

PRT;

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NOUSE PRELIMINARY; PRT; 159 AA.
299M58;
11-JUN-2001, integrated into UniProtKB/TrEMBL.
21-JUN-2001, sequence version 1.
27-FEB-2006, entry version 17.
27-FEB-2006, nonna-damage-inducible 45 gamm
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30-MAY-2000, integrated into Unil
11-NOV-1999, sequence version 1.
37-FEB-2006, entry version 22.
3rowth arrest and DNA-damage-ind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arose spontaneously;
HEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                            3ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
4ammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
4uroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [MRNA].

VEDLINE=99198964; PubMed=10100865; DOI=10.1016/S0014-5793(99)00234-3; Sojima S., Mayumi-Matsuda K., Suzuki H., Sakata T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Euarchontoglire
Muroidea; Muridae; Murinae; Rattus.
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                                                                                STRAIN=CZECH
                                                                                                                                       VCBI_TaxID=10090;
                                                                                                                                                                                                                            Yus musculus (Mouse)
                                                                                                                                                                                                                                                 Vame=Gadd45g;
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Pfam; PF01248; Ribosomal_L7Ae; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB020978; BAA78094.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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"Molecular cloning of rat GADD45gamma, gene induction and its role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VCBI_TaxID=10116;
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1 159 Growth arrest and DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LISNPHEDTWKDPALEKLSLFCEESRSFNDWVPSITLPE 159
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                                                                       SEQUENCE.
CH II; TISSUE=Mammary tumor metastatized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159
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Euarchontoglires; Glires;
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Pred. No. 2.3e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                    Sciurognathi;
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse of than Septembers of the stan 15,000 full-length human
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                                                                          07-MAR-2006, integrated into UniProtKE 07-MAR-2006, sequence version 1. 07-MAR-2006, entry version 1. Hypothetical protein. Bos taurus (Bovine). Eukaryota, Metazoa, Chordata; Craniata Mammalia; Eutheria; Laurasiatheria; Ce
                                                                                                                                                                                                                                                                                                                                                                           X1_BOVIN
Q2KIX1_BOVIN
Q2KIX1;
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MGI; MG
GO; GO;
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Pfam; PF01248; Ribosomal_L7Ae; 1.
SEQUENCE 159 AA; 17317 MW; C959
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    Pecora; Bovidae; NCBI_TaxID=9913;
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GO:0005634; C:nucleus; TAS.
GO:0005515; F:protein binding; IPI.
GO:0000518; F:activation of MAPKK activity; IDA.
GO:0000186; P:activation of MAPKK activity; TAS.
GO:00042095; P:interferon-gamma biosymthesis; TAS.
GO:0006469; P:negative regulation of protein kinase activity;
GO:0000074; P:regulation of progression through cell cycle; IGO:00045063; P:T-helper 1 cell differentiation; TAS.
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                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
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Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y., Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C. Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J. Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D., Siddiqui A., Holt R., Jones S.J., Marra M.A.; Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
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01-MAY-1999, sequence version
07-FEB-2006, entry version 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           responsive protein CR6).
Name=Gadd45g; Synonyms=Cr6;
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Hereford;
                                                                                                                                                                                                                                                                                                                     MEDLINE=99422022; PubMed=10490824; DOI=10.1038/sj.onc.1202885; Zhang W., Bae I., Krishnaraju K., Azam N., Fan W., Smith K., Hoffman B., Liebermann D.A.; "CR6: a third member in the MyD118 and Gadd45 gene family which functions in negative growth control."; Oncogene 18:4899-4907(1999).
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95.6%;
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Pred. No. 3.7e-68
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RA Hayashizaki Y.;
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EMBL; AK002237; BAB21955.1; -; mRNA.

Ensembl; ENSMUSG00000021453; Mus musculus.

MGI; MGI:1346325; Gadd459.

GO; GO:0005634; C:nucleus; TAS.

GO; GO:0005515; F:protein binding; IPI.

GO; GO:0000186; P:activation of MAPKK activity; IDA.

GO; GO:00042095; P:interferon-gamma biosynthesis; TAS.

GO; GO:000649; P:negative regulation of protein kinase activity; ID

GO; GO:000074; P:regulation of progression through cell cycle; IDA.

GO; GO:004503; P:T-helper 1 cell differentiation; TAS.
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    -!- FUNCTION: Involved in the regulation of growth and apoptosis.
    Mediates activation of stress-responsive MTK1/MEKK4 MAPKKK.
    -!- SIMILARITY: Belongs to the GADD45 family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004038; Ribosomal_L7A.
Pfam; PF01248; Ribosomal_L7Ae; 1.
Apoptosis; Developmental protein; Differentiation
                                                               121
121
                                                                                                                                                                                                                                                                                                                                                                                                                                152;
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                                                                                                                                                                            VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI
                                         LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
                                                                                                                                                                                                                                                                                 MTLEEVRGQDTVPESTARMQGAGKALHELLLSAHGQGCLTAGVYESAKVLNVDPDNVTFC
                                                                                                                               VLAADEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGADEEGGAPGDLHCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 787; DB 1; L
Pred. No. 1.7e-67;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth arrest and DNA-damage-inducible protein GADD45 gamma. protein GADD45 gamma. /FTIGLEPO 0000148337. 4B5996927C57988F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome.";
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RESULT 10 Q5VZ88_HUMAN

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"Expression and Regulation of Growth Arrest and DNA-damage-inducible "Expression and Regulation of Growth Arrest and DNA-damage-inducible protein GADD45 in the Chicken Ovary.";
submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          22HZD5_CHICK PRELIMINARY; PR
22HZD5;
37-MAR-2006, integrated into Uni
37-MAR-2006, sequence version 1.
37-MAR-2006, entry version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jrowth arrest and DNA-damage-inducible,
Vame=GADD45G; ORFNames=RP11-260L6.1-002;
Jomo Bapiens (Human)
                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cy Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-PEB-2006, entry version 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25VZ88_HUMAN PRELIMINARY; PRT; 141 AA.
25VZ88;
27-DEC-2004, integrated into UniProtKB/TrEMBL.
                                     :y Match
                                                                          EQUENCE 159
                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                             VUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                 VCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                Gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Frowth arrest and DNA-damage-inducible protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFCVLAAGEEDEGDIALQIHF
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                                                                          ΑΑ,
                                                                                               ABC88380.1;
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                                                                          88380.1; -; mRNA.
17411 MW; 97751B750876926F
                81.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.2%;
18;
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Pred. No. 9.7e-63;
                Score 675; DB 2
Pred. No. 1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UniProtKB/TrEMBL.
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                                                                              CRC64;
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Indels
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QBUUP4_XENLA

ID OBUUP4;

OBUUP4;

OC QBUUP4;

OC QBUAR-2002, sequence version 14.

DE XGAd45-gamma protein.

GN Name=xgad445-gamma protein.

RN NUCLEOTIDE SEQUENCE.

RN NUCLEOTIDE SEQUENCE.

RN NUCLEOTIDE SEQUENCE.

RN NUCLEOTIDE SEQUENCE.

RN Gomez-Skarmeta J.L.;

RN Gomez-Skarmeta J.L.;

RN NUCLEOTIDE SEQUENCE.

RN TISSUB=Whole;

RN MEDLINE=22341132; pubMed=1245491

RN MEDLINE=22388257; pubMed=1245491

RN MEDLINE=22388257; pubMed=124793

RN KILIANT-225:3884-391(2002).

RN NUCLEOTIDE SEQUENCE.

RN NUCLEOTIDE SEQUENCE.

RN NUCLEOTIDE SEQUENCE.

RN TISSUB=whole;

RN TISSUB=whole;

RN TISSUB=whole;

RN TISSUB=whole;

RN Altichenko L., Marustina K., Farm RA Klausner R.D., Collina F.S., Wace RA Altschul S.F., Zeeberg B. Buetc RA Hopkins R.F., Jordan H., Woore I RA Strausberg R.L., Feingold E.A., RA Klausner R.D., Collina F.S., Wace RA Altschul S.F., Jordan H., Woore I RA Distribenko L., Marustina K., Farm RA Raha S.S., Loquellano N.A., Petc RA Bosak S.A., McBenn P.J., WcKerna RA Brownstein M.J., Usdin T.B., Toe RA Godriguez A.C., Grimwood J., Sche RA Gomerch A., Schein J.E., Jones Generch A., Schein J.E., Jones Generation and initial analyssis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
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                                                                    RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R. Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.

MEDILINE=22274402; PubMed=12385755; DOI=10.1016/S0925-4773(02)00296-4;

De la Calle-Mustienes E., Glavic A., Modolell J., Gomez-Skarmeta J.;

"Xiro homeoproteins coordinate cell cycle exit and primary neuron formation by upregulating neuronal-fate repressors and downregulating the cell-cycle inhibitor XGadd45-gamma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=xgadd45-gamma;
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic and genomic tools for Xenopus research: initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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               99:16899-16903 (2002)
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MEDILIBE-2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 13
3 XENTR
26DIJ3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ry Match
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EMBL; BC078567; AAH78567.1; -; mRNA.
InterPro; IPR004038; Ribosomal L7A.
Pfam; PF01248; Ribosomal L7Ae; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein S., Gerhard D.S.; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-AUG-2004, sequence version 07-FEB-2006, entry version
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  Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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RESULT 14
Q7ZXC4 XENLA
ID Q7ZXC4, XENLA
Q7ZXC4
AC Q7ZXC4;
DT Q1-JUN-2003, E
DT 01-JUN-2003, E
DT 01-JU
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                                                                                                                                                                                                                                                                             RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., PrangelC.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., PrangelC.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT and mouse cDNA sequences.";

PLOCON MART M.S. MORLES S. Marchen M.S.,

RA Scherch R. M. Schein J.E., Jones S.J.M., Marra M.A.;

RT and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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InterPro; IPR004038; Ribosomal L7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.unipronderivs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                 Klein S.L., Strausberg Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGC53682 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003, sequence version
                                                                                                                                                                       TISSUE=Embryo;
                                    "Genetic and genomic tools
                                                                                                                                   MEDLINE=22341132;
                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122;
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AA; 17754 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                  PubMed=12454917; DOI=10.1002/dvdy.10174;
berg R.L., Wagner L., Pontius J., Clifto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.9%;
76.7%;
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                                          for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                99:16899-16903 (2002)
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.7e-54;
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Strausberg R. L., Peingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
iopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
iatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
srownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
aha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
sosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
ichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
illalan D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
inting M., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,
hiting M., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         denopus laevis (African clawed frog).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
denopodinae; Xenopus; Xenopus.
GDI_TaxID=8355;
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EnterPro; IPR004038; Ribosomal_L7A.

Pfam; PF01248; Ribosomal_L7Ae; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
dein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGC53682 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2005, sequence version 17-FEB-2006, entry version 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PISSUE=Brai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                           CISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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AA; 17771 MW;
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Pred. No. 2.1e-54;
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Butterfield Y.S.N., Krzywinski M.I., Staka U., Smailus D.E.,
Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
                                                                                                                                                                                                                                         EMBL; BC106626; AAI06627.1; -; mRNA.
InterPro; IPR004038; Ribosomal LTA.
Pfam; PF01248; Ribosomal LTAe; 1.
SEQUENCE 159 AA; 1771 MW; 7E252
                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                          Klein S., Gerhard D.S.;
Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                  121 LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
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                                                                                      61 VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI
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                                                                                                                                                   1 MTLEEVRGQDTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC
                                                                                                                                                                                               Similarity
 ILAADEYDEGDIALQIHFTLIQAFCCENDINIVRLNDTEKVAQILGFTDESAEPKDLHCI
                                                                                                                     Gerhard D.S.;
                                                                                                                                                                                  Conservative
                                                                                                                                                                                               77.7%;
                                                                                                                                                                                  17;
                                                                                                                                                                                               Score 642; DB 2;
Pred. No. 1.6e-53;
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Search completed: June 2, 2006, 22:36:46 Job time: 147 secs

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seq length: 2000000000
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826
Match Length
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Gapop 10.0 , Gapext 0.5
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| / EMC Celerra SIDS3/ptodata/2/iaa/5_COMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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Listing first 45
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
DB
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US-08-462-390B-12
US-08-463-074B-12
US-08-463-074B-12
US-08-463-08-463-12
US-08-652-446-12
US-09-534-811-7
US-09-994-016-9744
US-08-6797-831A-1
US-09-8797-831A-1
US-09-879833-2
US-09-600-158-7
US-09-534-811-7
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9744, Ap
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US-08-463-081B-12
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Patent No. 5871960 5837487
GENERAL IMFORMATION:
GENERAL IMFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression
NUMBER OF SEQUENCES: 35
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 Query Match
Best Local Similarity
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104	104	120	120	123	123	126	126	143	143	146.5	157	157	164	164	184	184	200	200
12.6	12.6				14.9	15.3	15.3	17.3	17.3	17.7	19.0	19.0	19.9	19.9	22.3	22.3	24.2	24.2
34	34	26	26	27	27	34	34	34	34	57	36	36	38	38	41	41	46	46
ω	N	w	N	w	N	w	N	W	N	N	w	N	ω	N	W	N	w	N
US-10-600-158-12	US-09-534-811-12	US-10-600-158-22	US-09-534-811-22	US-10-600-158-23	US-09-534-811-23	US-10-600-158-11	US-09-534-811-11	US-10-600-158-10	US-09-534-811-10	US-09-513-999C-6287	US-10-600-158-31	US-09-534-811-31	US-10-600-158-17	US-09-534-811-17	US-10-600-158-32	US-09-534-811-32	US-10-600-158-16	US-09-534-811-16
Sequence 12, Appl	Sequence 12, Appl	Sequence 22, Appl	Sequence 22, Appl	•		, t	11,	Sequence 10, Appr	•	α	Sequence 31, Appr	. L	1	;	32,		, to	Sequence 16, Appl

ALIGNMENTS

Thereof

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-463-081B-12
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
APPLICATION INFORMATION:
NAME: VIVIANA AMZe1, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                          TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower St. - Suite 1900
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CITY: Los Angeles
STATE: California
                                                                                                            H: 159 amino acids
amino acid
OGY: linear
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Score 826; DB 1;
Pred. No. 6.8e-93;
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                     Length 159;
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APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-UNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: & 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Anzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                  TELEFAX: (610)470-0701
FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acid
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                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                             VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI
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LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
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R. Nucleic Acids Encoding CRS Polypeptide,

R. Vector and Transformed Cell Thereof, and

R. Expression Thereof

S: 35
                                                                                                                                                                        100.0%; Score 826; DB 1; 100.0%; Pred. No. 6.8e-93;
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US-08-463-074B-12
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              Sequence 12, Application US/08463074B Patent No. 6020155
GENERAL INFORMATION:
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Best Local S
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RESULT 3
US-08-462-3908-12
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Patent No. 5882894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Smith, K. A., & Beadling, C.

TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector

TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereo

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION UNWBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUWBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUWBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (610)407-070 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Viviana Amzel, Ph. D. REGISTRATION NUMBER: 30,930 REFERENCE/DOCKET NUMBER: DAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Valley Forge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                      121 LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
121 LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
                                                                                                                                                                                                                                                        159;
                                                                                                        61 VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI
                                                                                                                                                               1 MTLEEVRGODTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC
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                                                                                                                                                                                                                                                   h 100.0%; Score 826; DB 1; Similarity 100.0%; Pred. No. 6.8e-93; 59; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI
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Thereof
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Smith,

Kendall A.

& Beadling,

Carol

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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074
FILING DATE: 5-JUN-1995
                                                                                                                                             ENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression There
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESSEE: (B) STREET: 444 South Flower St.
                                                                                                                                                                                                                                     quence 12, Application US/08465585C
                                                                                                                                                                                                                                                                              9-465-585C-12
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APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
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t Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY ACENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -463-074B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                               CORRESPONDENCE ADDRESS
COMPUTER READABLE FORM:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                 COUNTRY:
                                                                                            ADDRESSEE:
                                                                                                             ADDRESSEE:
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Conservative 0
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                                                                                          PRETTY, SCHROEDER & POPLAWSKI
(B) STREET:
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Pred. No. 6.8e-93;
; Mismatches 0;
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; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-465-585C-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (213) 622-7700
TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 12
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5
TITLE OF INVENTION: Polypeptide, Vector and Transformed
TITLE OF INVENTION: Expression Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/465,585C FILING DATE: 5-JUNE-1995 PRIOR APPLICATION NUMBER: USSN 08/330,108 APPLICATION NUMBER: USSN 08/330,108 FILING DATE: 27-OCT-1994
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
                                                              SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 826; DB 2; Local Similarity 100.0%; Pred. No. 6.8e-93; nes 159; Conservative 0; Mismatches nes
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COMPUTER: IF
                                                                                                                                                                                                                                                     STATE: California
                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                     COUNTRY:
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                                             US/08/652,446
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Suite 190

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 5-JAN

5-JAN-1998 JMBER: PCT 5-JUN-1996

EP App. # 96921319.8 1998 PCT/US/96/09194

APPLICATION NUMBER:

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PLICANT:
                                                                      BERAL INFORMATION:
PLICANT: Wang, Xin Wei
PLICANT: Harris, Curtis C.
PLICANT: Pornace Jr., Albert J.
PLICANT: Coursen, Jill D.
                                                                                                                                                                                              nence
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FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
                                                                                                                                                                          uence 7, Application ent No. 6613318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
                                                                                                                                                                                                                  -534-811-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein -652-446-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELECOMMUNICATION INFORMATION:
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FILING DATE: 5-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                   121 LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
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Zhan, Qimin
The Government of the United States of America as represented by the Secretary of the Department of Health and Human Services
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 826; DB 2; ilarity 100.0%; Pred. No. 6.8e-93; Conservative 0; Mismatches 0;
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5-JUN-1995
                                                                                                                                                                                                US/09534811
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; OTHER INFORMATION: human growth arrest and ; OTHER INFORMATION: protein (hGADD45gamma) US-10-600-158-7
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                                                                                                                                                SEQ ID NO 7
LENGTH: 159
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US/09/534,811
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,069
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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Matches
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Matches 159;
                       Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
FILE REFERENCE: 015280-367100US
CURRENT APPLICATION NUMBER: US/09/534,811
CURRENT FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,069
PRIOR APPLICATION NUMBER: US 60/126,069
PRIOR PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-25
PRIOR SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Xin Wei
APPLICANT: Harris, Curtis C.
APPLICANT: Fornace Jr., Albert
APPLICANT: Coursen, Jill D.
APPLICANT: Zhan, Qimin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: The Government of the United States of America APPLICANT: as represented by the Secretary of the APPLICANT: Department of Health and Human Services TITLE OF INVENTION: Methods for Identifying Inhibitors of TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of TITLE REFERENCE: 015280-367100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 159
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5. 7005419
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                       Similarity
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  Conservative
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100.0%; Pred. No. 6.8e-93;
tive 0; Mismatches 0;
                    100.0%; Score 826; DB 3; 100.0%; Pred. No. 6.8e-93;
0;
  Mismatches
                                                                                                                                    DNA-damage-inducible
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  Indels
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of Such
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Gaps
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PLICANT: VENTER, J. Craig et al.

TLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TLE REFERENCE: CL001307

RERENT FILING DATE: 2000-04-14

TOR APPLICATION NUMBER: US/09/949,016

RRENT FILING DATE: 2000-10-20

PLOR FILING DATE: 2000-10-20

PLOR FILING DATE: 2000-10-03

RIOR FILING DATE: 2000-10-03

RIOR APPLICATION NUMBER: 60/237,768

RIOR FILING DATE: 2000-10-03

RIOR FILING DATE: 2000-09-08

RIOR FILING DATE: 2000-09-08

RIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                           quence 1, Application US/08797831A
ent No. 5808031
:NERAL INFORMATION:
APPLICANT: Mikio, SUZUKI
APPLICANT: Takeshi, WATANABE
APPLICANT: TSUTOML, FUJIWARA
TITLE OF INVENTION: GRP17 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MBER OF SEQ ID NOS: 207012
DFTWARE: FastSEQ for Windows Version 4.0
DID: 09744
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--797-831A-1
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9-949-016-9744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 165
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                              COUNTRY: United States
                                                                                                                             STREET:
                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                20037-3202
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                                                                                                                                                                                                                                                                                                                                             Application US/08797831A
                                                                                                                           E: Sughrue, Mion, Zinn, Macpeak & Seas 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 7.2e-93;
, Mismatches 0;
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                                                                                                                                                                                                                                                                          ; LENGTH: 160
TYPE: PRT
ORGANISM: HL60 cell line
US-09-879-833-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09879833 Patent No. 6573371
                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2
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                                                                                                                                                                                                      Matches 157;
                                                                                                                                                                                                                       Query Match 98.2%;
Best Local Similarity 98.7%;
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Park, Chong-Hun; SAMYANG GENEX CORPORATION

IITLE OF INVENTION: CANCER DIAGNOSIS METHOD USING CELL GROWTH INHIBITING AND CELL DI

TITLE OF INVENTION: FERENTIATION SPECIFIC SYG972 GENE AND GENOMIC DNA AND PROMOTER

TITLE OF INVENTION: EREOF

FILE REFERENCE: PA/SYG/99601

CURRENT APPLICATION NUMBER: US/09/879,833

CURRENT FILING DATE: 2001-06-12

PRIOR APPLICATION NUMBER: KR 54933

PRIOR FILING DATE: 1998-12-12

PRIOR APPLICATION NUMBER: KR 63958

PRIOR FILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 3

SOFTWARE: KOPATIN 1.5
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INFORMATION FOR SEQUENCE CHARACTERISTICS
SEQUENCE CHARACTERISTICS
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SOFTWARE: Patent In
CURRENT APPLICATION DA
APPLICATION NUMBER:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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121 LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
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amino acid
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                                                                                                                            MTLEEVRGQDTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVRFC
                                                        VLAAGEEVEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI
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-534-811-2

uence 2, Application US/09534811

ent No. 6613318
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APPLICANT: Cocks, Benjamin Graeme
APPLICANT: Au-Young, Janice
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: NOVEL HUMAN MYELOID TERMINAL
TITLE OF INVENTION: DIFFERENTIATION RESPONSE GENE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2:
APPLICATION NUMBER: 08/2:
FILING DATE: 02-FEB-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0054 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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STATE: CA
                                                                                                                                                                                                                                                                                                                                       Local
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FILING DATE: Filed Herewith
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                                                                                                                                                                                                                                                                    1 MTLEEVRGQDTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC
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                                                                                                            OPPDIHCVLVTNPHSSQWKDPALSQLICFCRESRYMDQWVPVINLPE 164
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                                                                                                                                                                                 LLAADEDDDRDVALQIHFTLIQAFCCENDINILRVSNPGRLABULLLETDAGPAASEGAE 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
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Sequence 3, Application US/09208206 Patent No. 6913891 GENERAL INFORMATION:
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APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
FILE REFERENCE: 015280-367100US
CURRENT APPLICATION NUMBER: US/09/534,811
CURRENT FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Harris, Curtis C.
APPLICANT: Fornace Jr., Albert J.
APPLICANT: Coursen, Jill D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/208,206
FILING DATE: 09-Dec-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seilhamer, Jeffrey J.
TITLE OF INVENTION: NOVEL HUMAN MYELOID TERMINAL
DIFFERENTIATION RESPONSE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cocks, Benjamin Graeme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 OPPDIHCVIVTNPHSSOWKDPALSQLICFCRESRYMDOWVPVINLPE 164
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APPLICATION NUMBER: US/08/602,208 FILING DATE: 15-FEB-1996 APPLICATION NUMBER: 08/221,531 FILING DATE: 02-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S. ZIP: 94303
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ATTORNEY/AGENT INFORMATION:

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PLICANT: Chan, Qimin
PLICANT: The Government of the United States of America
PLICANT: The Government of the Secretary of the
PLICANT: as represented by the Secretary of the
PLICANT: Department of Health and Human Services
TLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
TLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
ERRENT APPLICATION NUMBER: US/10/600,158
PREENT APPLICATION NUMBER: US/10/600,158
PREENT FILING DATE: 2003-06-20
RIOR APPLICATION NUMBER: US/09/534,811
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SEQUENCE CHARACTERISTICS:
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st Local Similarity
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                                                                                                                                                                                                                                                                                                                                         PELICANT: Wang, Xin Wei
PELICANT: Harris, Curtis C.
PPLICANT: Fornace Jr., Albert J.
PPLICANT: Coursen, Jill D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quence 2, Application US/10600158 ent No. 7005419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 LLAADEDDRDVALQIHFTLIQAFCCENDINILRVSNPGRLAELLLLETDAGPAASEGAE 117
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Copyright (c) 1993 - 2006 Biocceleration Ltd.

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US-10-287-436A-11127
US-10-631-467-560
US-10-621-234-1127
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Sequence 176, Appl
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                         Sequence 10, Application US/10626905
publication No. US20040121463A1
GENERAL INFORMATION:
APPLICANT: FRANZOSO, GUIDO
APPLICANT: DESMABLE, ENRICO
APPLICANT: ZAZZERONI, FRANCESCA
APPLICANT: PAPA, SALVATORE
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OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS

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LE REFERENCE: 21459-94575

RRENT APPLICATION NUMBER: US/10/626,905

RRENT FILING DATE: 2003-07-25

IOR APPLICATION NUMBER: PCT/US02/31548

IOR FILING DATE: 2002-10-02

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IOR APPLICATION NUMBER: 10/263,330
IOR FILING DATE: 2002-10-02
IOR APPLICATION NUMBER: 60/328,811
IOR FILING DATE: 2001-10-12
IOR APPLICATION NUMBER: 60/326,492
IOR FILING DATE: 2001-10-02
WHER OF SEQ ID NOS: 53
FTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
TLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT
TLE OF INVENTION: RHEUMATOID ARTHRITIS
(LE REFERENCE: 10872.514696
ARENT APPLICATION NUMBER: US/10/287,436A
RRENT FILING DATE: 2002-10-31
IOR APPLICATION NUMBER: US 60/336,220
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IOR FILING DATE: 2001-10-31
"HBER OF SEQ ID NOS: 1446
FTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                               RGANISM: Homo sapiens
-287-436A-441
                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                              ID NO 441
ENGTH: 159
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                      121 LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
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LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
                                                                                      VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI
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APPLICATION NUMBER: JP 2002-229312
PRIOR FILING DATE: 2003-00-6
PRIOR FILING DATE: 2003-03-12
PRIOR FILING DATE: 2003-03-12
PRIOR FILING DATE: 2003-03-07-31
PRIOR APPLICATION NUMBER: UP 2003-077212
PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR APPLICATION NUMBER: JP 2002-229312
PRIOR APPLICATION NUMBER: JP 2002-29312
PRIOR APPLICATION NUMBER: JP 2002-229312
PRIOR APPLICATION NUMBER: JP 2002-229312
PRIOR FILING DATE: 2003-03-00
PRIOR FILING 
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US-10-287-436A-1142
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Publication No. US200S0202421A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
TITLE REFERENCE: 10872.514696
FILE REFERENCE: 10872.514696
CURRENT APPLICATION NUMBER: US/10/287,436A
CURRENT APPLICATION NUMBER: US/10/336,220
PRIOR APPLICATION NUMBER: US 60/336,220
PRIOR FILLING DATE: 2001-10-31
PRIOR FILLING DATE: 2001-10-31
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Publication No. US20
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1142
LENGTH: 159
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Best Local :
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100.0%; Pred. No. 3e-87;
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LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159

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PPLICANT: Andarmani, Susan

"PPLICANT: Tang, Y. Tom

"TIE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

"LE REFERENCE: 821A

"RRENT APPLICATION NUMBER: US/10/821,234

"RRENT FILING DATE: 2004-04-07

"IOR APPLICATION UNUMBER: US 60/462,047

"IOR FILING DATE: 2003-04-07

"MBER OF SEQ ID NOS: 1704

"MBER OF SEQ ID NOS: 1704
                                                                                                                                                                                               PERAL INFORMATION:

PRICANT: Park, Chong-Hun; SAMYANG GENEX CORPORATION

PPLICANT: Park, Chong-Hun; SAMYANG GENEX CORPORATION

TLE OF INVENTION: CANCER DIAGNOSIS METHOD USING CELL GROWTH INHIBITING AND CELL DIF

TLE OF INVENTION: ERRENTIATION SPECIFIC SYG972 GENE AND GENOMIC DNA AND PROMOTER 1

TLE REPERENCE: PA/SYG/99601

TREBET APPLICATION NUMBER: US/09/879,833

TREBIT FILING DATE: 2001-06-12

ZIOR APPLICATION NUMBER: KR 54933

ZIOR FILING DATE: 1998-12-12

ZIOR APPLICATION NUMBER: KR 63958

ZIOR APPLICATION NUMBER: KR 63958

ZIOR FILING DATE: 1998-12-30

TMBER OF SEQ ID NOS: 3
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  st Local Similarity
sches 157; Conserv
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-821-234-1127
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                                                                                                                                                                  . ID NO 2
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                                                                                 RGANISM: HL60 cell line
                                                                                                                                                                                     FTWARE: KOPATIN 1.5
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Score 811; DB 3;
Pred. No. 1.7e-85;
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TITLE OF INVENTION: MODULATORS OF APOPTOSIS
FILE REFERENCE: ARCD:379USP1
CURRENT APPLICATION NUMBER: US/10/263,330
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US/60/326,492
PRIOR FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: FRANZOSO, GUIDO
APPLICANT: DESMAELE, ENRICO
APPLICANT: ZAZZERONI, FRANCESCA
APPLICANT: PAPA, SALVATORE
APPLICANT: PAPA, SALVATORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Appublication No.
                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 159
                    121 LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
                                                                                                                                                                                                                                                           152;
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                                                                                61 VLAADEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGADEEGGAPGDLHCI
                                                                                                         61 VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI 120
                                                                                                                                                                    1 MTLEEVRGODTVPESTARMQGAGKALHELLLSAHGQGCLTAGVYESAKVLNVDPDNVTFC
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LISNPNEDTWKDPALEKLSLFCEESRSFNDWVPSITLPE 159
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                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                         Score 787; DB 4
Pred. No. 1e-82;
0; Mismatches
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RESULT 9
US-10-626-905-12
US-10-626-905-12
; Sequence 12, Application US/10626905
; Publication No. US20040121463A1
; GENERAL INFORMATION:
   APPLICANT: PARAVEOSO, GUIDO
   APPLICANT: DESMAELE, ENRICO
   APPLICANT: DESMAELE, ENRICO
   APPLICANT: PAPA, SALVATORE
   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS
   FILE REFERENCE: 21459-94575
; CURRENT APPLICATION NUMBER: US/10/626,905
; CURRENT FILING DATE: 2003-07-25
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2002-10-02
; PRIOR FILING DATE: 2001-10-12
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Jence 1387, Application US/10631467
lication No. US20050208496A1
3RAL INFORMATION:
PLICANT: Genox Research Inc.
FILE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive price of INVENTION: disease
LE REFERENCE: 3462.1005-000
RENT APPLICATION NUMBER: US/10/631,467
RENT FILING DATE: 2003-07-31
IOR APPLICATION NUMBER: UP 2003-077212
IOR FILING DATE: 2003-03-20
IOR APPLICATION NUMBER: UP 2002-229312
IOR FILING DATE: 2002-08-06
**MBER OF SEQ ID NOS: 2086
FTWARE: Patentin version 3.1
ID NO 1387
STED. TOTAL
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IOR FILING DATE: 2001-10-02
WHER OF SEQ ID NOS: 53
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t Local Similarity
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-087-192-1356 Application US/10087192 lication No. US20020182586A1 BRAL INFORMATION:
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Similarity 95.6%;
52; Conservative
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Pred. No. 1e-82;
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Pred. No. 1e-82;
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APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
FITTLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
FITLE OF INVENTION: CANCER
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US/09/747,377
PRIOR APPLICATION NUMBER: US/09/747,377
PRIOR APPLICATION NUMBER: US/09/747,377
PRIOR APPLICATION NUMBER: US/09/748,586
PRIOR APPLICATION NUMBER: US/09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER: OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1353
LENGTH: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND ME'
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 1356
LENGTH: 141
TYPE: PRT
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US-10-087-192-1356
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Matches
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Best Local Similarity
Matches 136; Conserv
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                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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Local Similarity 100.0%; I
hes 141; Conservative 0;
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SLFCEESRSVNDWVPSITLPE
                                                               TLIQAFCCENDIDIVRVGDVQRLAAIVGADEEGGAPGDLHCILISNPNEDTWKDPALEKL
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                                                                                                                                                                                                                             Score 710; DB 4;
Pred. No. 8.7e-74;
0; Mismatches 5
                         159
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138

SLFCEESRSFNDWVPSITLPE 158

nuence 176, A lication No. 0-617-316-176

Application US/10617316 o. US20050130263A1

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FERAL INFORMATION:

PLICANT: Havukkala, Ilka J

PLICANT: Glenn, Matthew

PLICANT: Grigor, Murray R.

PLICANT: Molenaar, Adrian J.

PLICANT: Molenaar, Adrian J.

PLICANT: Molenaar, Adrian J.

PLICANT: Molenaar, Adrian J.

PLICANT: Molenaar, Gland and Methods Follows Foll

Bovine For Their Use.

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PPLICANT: ZAZZERONI, FRANCESCA
PPLICANT: ZAZZERONI, FRANCESCA
PPLICANT: PAPA, SALVATORE
THE OF INVENTION: MODULATORS OF APOPTOSIS
THE REFERENCE: ARCD:379USP1
RRENT APPLICATION NUMBER: US/10/263,330
RRENT FILING DATE: 2002-10-02
RIOR FILING DATE: 2001-10-02
PIOR FILING DATE: 2001-10-02
PRENT FOR PRICH SOURCE STATES SEED NOS: 15
PRENT OF SEQ ID NOS: 15
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lication No. US20030077262A1
                                                                                                                                         ery Match
                                                                                                                                                                                           0-263-330-6
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PLICANT: DESMAELE, ENRICO
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                                                                                                                                                                                                              RGANISM: Homo sapiens
                                                                                                                                                                                                                                                              ENGTH: 165
                                                                                                                                                                                                                                                                                       ID NO 6
                                                                                                                     Local Similarity
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                           1 MTLEEVRGQDTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC 60
MTLEEFSAGE---QKTERMDKVGDALEEVLSKALSORTITVGVYEAAKLLNVDPDNVVLC 57
                                                                                              Conservative
                                                                                         55.4%; Score 457.5; DB 4; 54.5%; Pred. No. 1.9e-44; ative 22; Mismatches 43;
                                                                                                                                           Length 165;
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CURRENT APPLICATION NUMBER: US/10/626,905
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: PCT/US02/31548
PRIOR APPLICATION NUMBER: PCT/US02/31548
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 10/263,330
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/328,811
PRIOR APPLICATION NUMBER: 60/328,811
PRIOR APPLICATION NUMBER: 60/326,492
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/326,492
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-02
Search completed: June
Job time : 180 secs
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Publication No. US20040121463A1
                                                                                                                                                                                                                                                                                                                                   Query Match 55.4%; Score 457.5; DB 4
Best Local Similarity 54.5%; Pred. No. 1.9e-44;
Matches 91; Conservative 22; Mismatches 43
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APPLICANT: DESMAELE, ENRICO
APPLICANT: ZAZZERONI, FRANCESCA
APPLICANT: PAPA, SALVATORE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 165
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                                                                                                                          113 APGDLHCILISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
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                                                                                     OPPDIHCVI/TUPHSSQWKDPALSQLICFCRESRYMDQWVPVINLPE 164
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                          2006,
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ery Match

65.5%;

Score 541; DB 5; I Pred. No. 2.2e-54; 2; Mismatches 2;

Length 110; Indels

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ORGANISM: Bovine 0-617-316-176

ENGTH: 110 YPE: PRT

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Gapop 10.0 , Gapext 0.5
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(without alignments)
204.318 Million cell updates/sec
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| RMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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Copyright (c) 1993 - 2006
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US-10-953-349-9815
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Sequence 7, Appli
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Sequence 16, Appl
Sequence 17, Appl
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Sequence 11, Appl
Sequence 11, Appl
Sequence 22, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 18, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 9815, Ap
Sequence 9816, Ap
Sequence 9816, Ap
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Sequence 9818, Appl
Sequence 19, Appl
Sequence 20, Appl
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Sequence 20461, A	-	o	13849,	Sequence 13850, A	Ø	Sequence 24, Appl	Sequence 2019, Ap	Sequence 2020, Ap	Sequence 2021, Ap	Sequence 21629, A		21630,	30065,	30066,		•	e 34/0,	e 26527,	Ф	

ALIGNMENTS

US-11-297-160-7

Sequence 7, Application US/11297160 Publication No. US20060088888A1

GENERAL INFORMATION

Xin Wei

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APPLICANT: Zhan, Qimin the United States of America APPLICANT: The Government of the United States of America APPLICANT: The Government of the Secretary of the APPLICANT: Department of Health and Human Services TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45 TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity FILE REPERENCE: 015280-367100US CURRENT APPLICATION NUMBER: US/11/297,160 CURRENT FILING DATE: 2005-12-07 PRIOR APPLICATION NUMBER: US/10/600,158 PRIOR FILING DATE: 2003-06-20 PRIOR FILING DATE: 2000-03-24 PRIOR APPLICATION NUMBER: US 60/126,069 PRIOR FILING DATE: 1999-03-25 NUMBER OF SEQ ID NOS: 32
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APPLICANT: Forna
APPLICANT: Cours
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Matches 15
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                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                            LENGTH: 159
TYPE: PRT
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human growth arrest and DNA-damage-inducible
OTHER INFORMATION: protein (hGADD45gamma)
                                                                                                                                                                                                                 159;
  121 LISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
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                                                                                                                                                  1 MTLEEVRGQDTVPESTARMQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFC 60
                                                                                                                                                                                                                                     Similarity
                                                                VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVGAGEEAGAPGDLHCI 120
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Fornace Jr., Albert J.
Coursen, Jill D.
                                                                                                                                                                                                                   Conservative
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100.0%; Pred. No. 5.5e-82;
tive 0; Mismatches 0;
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PLICANT: Zhan, Qinin

PLICANT: The Government of the United States of America

PLICANT: The Government of the Secretary of the

PLICANT: Department of Health and Human Services

PLICANT: Department of Health and Inhibitors of GADD45

PLICANT: Polypeptide Activity, and Inhibitors of Such Activity

PRENT APPLICATION NUMBER: US/11/297,160

PRENT FILING DATE: 2005-12-07

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'PLICANT: Harri
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TLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
LE REFERENCE: 28967/39178
REENT APPLICATION NUMBER: US/10/505,928
RRENT FILING DATE: 2004-08-27
IOR APPLICATION NUMBER: US 60/363,019
IOR FILING DATE: 2002-03-07
WBER OF SEQ ID NOS: 866
FTWARE: Patentin 3.2
                                                                                                                                                                            ID NO 2
ENGTH: 165
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RGANISM: Homo sapiens
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Fornace Jr., Albert J.
Coursen, Jill D.
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RESULT 5
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US-11-297-160-8
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APPLICANT: Harris, Curtis C.
APPLICANT: Fornace Jr., Albert J.
APPLICANT: Coursen, Jill D.
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Best Local Similarity
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: The Government of the United States of America APPLICANT: as represented by the Secretary of the APPLICANT: Department of Health and Human Services TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45 TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such FILE REFERENCE: 015280-367100US CURRENT FILLMG DATE: 2005-12-07 PRIOR APPLICATION NUMBER: US/10/600,158 PRIOR APPLICATION NUMBER: US/10/600,158 PRIOR APPLICATION NUMBER: US/10/600,158 PRIOR FILING DATE: 2003-06-20
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PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,069
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mus musculus
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                                                                                                                                                  58 LLAADEDDDRDVALQIHFTLIRAFCCENDINILRVSNPGRLAELLLLENDAGPAESGGAA
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91; Conservative
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; Sequence 6, Application US/11297160
; Publication No. US20060088888A1

Harris, Curtis C.
Fornace Jr., Albert J.
Coursen, Jill D.

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PPLICANT: Zhan, Qimin

PPLICANT: The Government of the United States of America

PPLICANT: The Government of the Secretary of the

PPLICANT: Department of Health and Human Services

TIE OF INVENTION: Methods for Identifying Inhibitors of GADD45

TIE OF INVENTION: Methods for Identifying Inhibitors of Such Activity

ILE REFERENCE: 015280-367100US

TRENT APPLICATION NUMBER: US/11/297,160

TRENT APPLICATION NUMBER: US/11/297,160

TRENT FILING DATE: 2005-12-07

RIOR APPLICATION NUMBER: US/01/600,158

RIOR APPLICATION NUMBER: US/09/534,811

RIOR APPLICATION NUMBER: US/09/534,811
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                                                                                                                                                                                                                                                                                                  PPLICANT: The Government of the United States of America
PPLICANT: as represented by the Secretary of the
PPLICANT: Department of Health and Human Services
TLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
TLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
LE REFERENCE: 015280-367100US
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                                                                                                TRRENT APPLICATION NUMBER: US/11/297,160
TRRENT FILING DATE: 2005-12-07
RIOR APPLICATION NUMBER: US/10/600,158
RIOR FILING DATE: 2003-06-20
RIOR APPLICATION NUMBER: US/09/534,811
RIOR FILING DATE: 2000-03-24
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PPLICANT: Harris, Curt
PPLICANT: Fornace Jr.,
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PIOR APPLICATION NUMBER: US 60/126,069
PIOR FILING DATE: 1999-03-25
PMBER OF SEQ ID NOS: 32
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Fornace Jr., Albert J.
Coursen, Jill D.
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CURRENT FILING DATE: 2005-12-07
PRIOR APPLICATION NUMBER: US/10/600,158
PRIOR FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US/09/534,811
PRIOR APPLICATION NUMBER: US/09/534,811
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,069
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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                                                                          Matches
                                                                                                             Query Match
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APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
FILE REFERENCE: 015280-3671007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, APPLICANT: Harr:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 16
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: rat growth arrest and DNA-damage-inducible OTHER INFORMATION: (rGADD45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:exemplary OTHER INFORMATION: peptide inhibiting GADD45-related dissociation OTHER INFORMATION: Cdc2/cyclin Bl complexes
                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 QTP-DLHCVLVTNPHSSQWKDPALSQLICFCRESRYMDQWVPVINLPE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 GAPGDLHCILISNPNEDAWKDPALEKLSLFCEESRSVNDWVPSITLPE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 LLAADEDDDRDVALQIHFTLIRAFCCENDINILRVSNPGRLAELLLLENDKSPAESGGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIV------GAGEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
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                        45 ESAKVLNVDPDNVTFCVLAAGEEDEGDIALQIHFTLIQAFCCENDI 90
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                                                                                                                                                                                                                                                                                           46
                                                                                              Similarity
Harris, Curtis C.
Fornace Jr., Albert J.
Coursen, Jill D.
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                                                                              Conservative
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                                                                                            24.2%;
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Pred. No. 4.6e-40;
                                                                            Score 200; DB 7;
Pred. No. 2.4e-15;
6; Mismatches 4
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                                                                                Indels
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PLICANT: Zhan, Qimin
PLICANT: The Government of the United States of America
PLICANT: as represented by the Secretary of the
PLICANT: Department of Health and Human Services
TLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
TLE OF INVENTION: Methods for Identifying Inhibitors of Such Activity
LE REFERENCE: 015280-367100US
REENT APPLICATION NUMBER: US/11/297,160
REENT FILING DATE: 2005-12-07
IOR APPLICATION NUMBER: US/000,158
IOR FILING DATE: 2003-06-20
IOR APPLICATION NUMBER: US/09/534,811
IOR PILING DATE: 2000-03-24
IOR APPLICATION NUMBER: US 60/126,069
IOR FILING DATE: 1999-03-25
TARRE SECO. TO NUMBER: US 60/126,069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IOR APPLICATION NUMBER: US/10/600,158
IOR FILING DATE: 2003-06-20
IOR APPLICATION NUMBER: US/09/534,811
IOR FILING DATE: 2000-03-24
IOR APPLICATION NUMBER: US 60/126,069
IOR FILING DATE: 1999-03-25
WHER OF SEQ ID NOS: 32
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PLICANT: Harris, Curtis C.
PLICANT: Fornace Jr., Albert J.
PLICANT: Coursen, Jill D.
MBER OF SEQ ID NOS: 32
FTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLICANT: Harris, Curtis C.
PLICANT: Fornace Jr., Albert J.
PLICANT: Coursen, Jill D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lication No. US200600888888A1
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PPLICANT: as represented by the Secretary of the
PLICANT: Department of Health and Human Services
TLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
TLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
TLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
TLE REFERENCE: 015280-367100US
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RGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLICANT: Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ry Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THER INFORMATION: Description of Artificial Sequence:exemplary THER INFORMATION: peptide inhibiting GADD45-related dissociation THER INFORMATION: Cdc2/cyclin B1 complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LNVDPDNVVLCLLAADEDDDRDVALQIHFTLIQAFCCENDI 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Conservative
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APPLICANT: Zhan, Qimin
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
TITLE OF INVENTION: Methods for Identifying Inhibitors of Such Activity
FILE REFERENCE: 015280-357100US
CURRENT APPLICATION NUMBER: US/11/297,160
CURRENT FILING DATE: 2005-12-07
PRIOR APPLICATION NUMBER: US/0600,158
PRIOR FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US/09/534,811
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1099-03-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                           Sequence 10, Application US/11297160
Publication No. US2006008888881
GENERAL INFORMATION:
APPLICANT: Wang, Xin Wei
APPLICANT: Fornace Jr., Albert J.
APPLICANT: Coursen, Jill D.
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US-11-297-160-10
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APPLICANT: Wang, Xin
APPLICANT: Harris,
APPLICANT: Fornace
APPLICANT: Coursen,
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US-11-297-160-31
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                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                55 DNVTFCVLAAGEEDEGDIALQIHFTLIQAFCCENDI 90
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Fornace Jr., Albert
Coursen, Jill D.
Zhan, Qimin
The Government of the United States of as represented by the Secretary of the
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No. US20060088888A1
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                                                                                                                                                                                                                                                                                                                                                                                              19.0%; Score 157; DB 7; 77.8%; Pred. No. 7.4e-11;
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Pred. No. 1.4e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 36;
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PPLICANT: Department of Health and Human Services
TILE OF INVENTION: Methods for Identifying Inhibitors of GADD45
TILE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity LE REFERENCE: 015280-367100US
TREBUT APPLICATION NUMBER: US/11/297,160
TRRENT FILING DATE: 2005-12-07
RICHER APPLICATION NUMBER: US/10/600,158
RIOR FILING DATE: 2003-06-20

EIOR APPLICATION NUMBER: US/09/534,811
RIOR FILING DATE: 2000-03-24
RIOR APPLICATION UNMBER: US 60/126,069
RIOR FILING DATE: 1999-03-25

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) ID NO 10
LENGTH: 34
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                                                                                                                                                                                                                                                                                                                                                       RIOR APPLICATION NUMBER: US/10/600,158
RIOR FILING DATE: 2003-06-20
RIOR APPLICATION NUMBER: US/09/534,811
RIOR FILING DATE: 2000-03-24
RIOR APPLICATION NUMBER: US 60/126,069
RIOR FILING DATE: 1999-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: The Government of the United States of America
PPLICANT: as represented by the Secretary of the
PPLICANT: Department of Health and Human Services
"TLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
"TLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
"LE REFERENCE: 015280-367100US
"RRENT APPLICATION NUMBER: US/11/297,160
"RRENT FILING DATE: 2005-12-07
"RRENT FILING DATE: 2005-12-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MBER OF SEQ ID NOS: 32
                                                                                                                                                      THER INFORMATION: Description of Artificial Sequence:human GADD4THER INFORMATION: residues 58-91 with residues 62-67 changed to THER INFORMATION: by site-directed mutagenesis (M62-67)
                                                                                                                                                                                                                                                                                                   .) ID NO 11
                                                                                                                                                                                                                                                                                                                        OMBER OF SEQ ID NOS: 32
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                                                                                                                                                                                                                     EATURE:
                                                                                                                                                                                                                                      RGANISM: Artificial Sequence
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                                                                               Similarity
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Fornace Jr., Albert J.
Coursen, Jill D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhan, Qimin
                                                            Conservative
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                                                                             15.3%;
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Pred. No. 2.2e-09;
                                                          Score 126; DB 7;
Pred. No. 1.5e-07;
4; Mismatches 6
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CURRENT FILING DATE: 2005-12-07
PRIOR APPLICATION NUMBER: US/10/600,158
PRIOR APPLICATION NUMBER: US/09/634,811
PRIOR APPLICATION NUMBER: US/09/534,811
PRIOR APPLICATION NUMBER: US/09/534,811
PRIOR APPLICATION NUMBER: US/09/534,811
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 32
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LENGTH: 27
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                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Xin Wei
APPLICANT: Harris, Curtis C.
APPLICANT: Fornace Jr., Albert J.
APPLICANT: Coursen, Jill D.
APPLICANT: Coursen, Jill D.
                                                                                                                           Best
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                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                   LENGTH: 27
TYPE: PRT
ORGANISM: Artificial Sequence
PERTURE:
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:exemplary
OTHER INFORMATION: peptide inhibiting GADD45-related dissociation
OTHER INFORMATION: Cdc2/cyclin Bl complexes
                                                                                                                           Local
                                   64 AGEEDEGDIALQIHFTLIQAFCCENDI 90
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ADEDDDRDVALQIHFTLIQAFCCENDI 27
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                                                                                                    Conservative
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                                                                                                                           14.9%;
81.5%;
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Pred. No. 2.3e-07;
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RESULT 14
US-11-297-160-22
US-11-297-160-22
Sequence 22, Application US/11297160
Publication No. US20060088888A1
GEMERAL INFORMATION:
APPLICANT: Wang, Xin Wei
APPLICANT: Fornace Jr., Albert J.
APPLICANT: Coursen, Jill D.
APPLICANT: Coursen, Jill D.
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
ITILE OF INVENTION: Methods for Identifying Inhibitors of Such Activity
FILE REFERENCE: 015280-367100US
CURRENT FILLNG DATE: 2005-12-07
PRIOR APPLICATION NUMBER: US/11/297,160
CURRENT FILLNG DATE: 2005-12-07
PRIOR APPLICATION NUMBER: US/09/534,811
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,069
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 32
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THER INFORMATION: Description of Artificial Sequence:exemplary
THER INFORMATION: peptide inhibiting GADD45-related dissociation of
THER INFORMATION: Cdc2/cyclin B1 complexes
h completed: June ime : 10 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'YPE: PRT
RGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                           THER INFORMATION: Description of Artificial Sequence:human GADD45
THER INFORMATION: residues 58-91 with residues 74-79 changed to Ala
THER INFORMATION: by site-directed mutagenesis (M74-79)
-297-160-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'YPE: PRT
|RGANISM: Artificial Sequence
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Similarity 84.0%;
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                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                          Score 104; DB 7; Pred. No. 3.5e-05;
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